



#19

CERTIFICATE OF MAILING (37 CFR 1.8 (a)).

I hereby certify that the attached papers or fee is being deposited with the United States Postal Service on the date shown below with sufficient postage as first class mail in an envelope addressed to: «INSERT» Assistant Commissioner For Patents, Washington, D.C.

December 6, 1996 Liza D. Hohenschutz
(Date) (Printed Name)

Liza D. Hohenschutz
(Signature)

ZENECA Inc.
Docket No. 70086

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Application of: WOOD ET AL

Serial No.: 08/669,656

Filed: JUNE 24, 1996

For: ION CHANNEL

Box Missing Part
Assistant Commissioner for Patents
Washington, DC 20231

Sir:

**STATEMENT TO SUPPORT FILING AND SUBMISSION
IN ACCORDANCE WITH 37 CFR §§1.821 THROUGH 1.825**

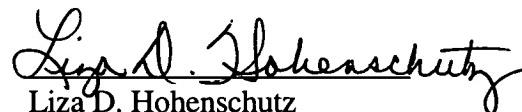
- (X) I hereby state, in accordance with the requirements of 37 C.F.R. §1.821(f), that the contents of the paper and computer readable copies of the Sequence Listing, submitted in accordance with the 37 C.F.R. §1.821(c) and (e), respectively are the same.
- () I hereby state that the submission filed in accordance with 37 C.F.R. 1.821(g) does not include new matter.
- () I hereby state that the submission filed in accordance with 37 C.F.R. §1.821(h) does not include new matter or go beyond the disclosure in the international application as filed.
- (X) I hereby state that the amendments, made in accordance with 37 C.F.R. §1.825(a), included in the substitute sheet(s) of the Sequence Listing are supported in the

application, as filed, at pages 50-105. I hereby state that the substitute sheet(s) of the Sequence Listing does (do) not include new matter.

- (X) I hereby state that the substitute copy of the computer readable form, submitted in accordance with **37 C.F.R. §1.825(b)**, is the same as the amended Sequence Listing.
- () I hereby state that the substitute copy of the computer readable form, submitted in accordance with **37 C.F.R. §1.85(d)**, contains identical data to that originally filed.

Respectfully submitted,

ZENECA INC.


Liza D. Hohenschutz
Attorney for Applicant(s)
Reg. No. 33,712
Telephone: 302/886-7466

Dated: December 6, 1996

SEQUENCE LISTING

(1) GENERAL INFORMATION:

5

(i) APPLICANT: Wood, John N.
Akopian, Armen N.

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(ii) TITLE OF INVENTION: Ion Channel

15

(iii) NUMBER OF SEQUENCES: 31

(iv) CORRESPONDENCE ADDRESS:

15

(A) ADDRESSEE: ZENECA Phamraceuticals
(B) STREET: 1800 Concord Pike, P.O. Box 15437
(C) CITY: Wilmington
(D) STATE: Delaware
(E) COUNTRY: USA
(F) ZIP: 19850

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(v) COMPUTER READABLE FORM:

25

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

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(vi) CURRENT APPLICATION DATA:

35

(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

40

(A) NAME: Hohenschutz, Liza D.
(B) REGISTRATION NUMBER: 33,712
(C) REFERENCE/DOCKET NUMBER: PHM.70086

(ix) TELECOMMUNICATION INFORMATION:

45

(A) TELEPHONE: (302) 886-7466

50

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 6524 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

55

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

60

(A) NAME/KEY: CDS
(B) LOCATION: 204..6077

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

65

TAGCTTGCTT CTGCTAATGC TACCCAGGC CTTTAGACAG AGAACAGATG GCAGATGGAG

60

TTTCTTATTG CCATGCGCAA ACGCTGAGCC CACCTCATGA TCCCGGACCC CATGGTTTC

120

AGTAGACAAC CTGGGCTAAG AAGAGATCTC CGACCTTATA GAGCAGCAA GAGTGTAAAT

180

	TCTTCCCCAA	GAAGAATGAG	AAG	ATG	GAG	CTC	CCC	TTT	GCG	TCC	GTG	GGA	230				
				Met	Glu	Leu	Pro	Phe	Ala	Ser	Val	Gly					
5				1					5								
	ACT	ACC	AAT	TTC	AGA	CGG	TTC	ACT	CCA	GAG	TCA	CTG	GCA	GAG	ATC	GAG	278
	Thr	Thr	Asn	Phe	Arg	Arg	Arg	Phe	Thr	Pro	Glu	Ser	Leu	Ala	Glu	Ile	Glu
10	10	15						20							25		
	AAG	CAG	ATT	GCT	GCT	CAC	CGC	GCA	GCC	AAG	AAG	GCC	AGA	ACC	AAG	CAC	326
	Lys	Gln	Ile	Ala	Ala	His	Arg	Ala	Ala	Lys	Lys	Ala	Arg	Thr	Lys	His	
15	30					35				35				40			
	AGA	GGA	CAG	GAG	GAC	AAG	GGC	GAG	AAG	CCC	AGG	CCT	CAG	CTG	GAC	TTG	374
	Arg	Gly	Gln	Glu	Asp	Lys	Gly	Glu	Lys	Pro	Arg	Pro	Gln	Leu	Asp	Leu	
20	45					50								55			
	AAA	GAC	TGT	AAC	CAG	CTG	CCC	AAG	TTC	TAT	GGT	GAG	CTC	CCA	GCA	GAA	422
	Lys	Asp	Cys	Asn	Gln	Leu	Pro	Lys	Phe	Tyr	Gly	Glu	Leu	Pro	Ala	Glu	
25	60					65								70			
	CTG	GTC	GGG	GAG	CCC	CTG	GAG	GAC	CTA	GAC	CCT	TTC	TAC	AGC	ACA	CAC	470
	Leu	Val	Gly	Glu	Pro	Leu	Glu	Asp	Leu	Asp	Pro	Phe	Tyr	Ser	Thr	His	
30	75					80								85			
	CGG	ACA	TTC	ATG	GTG	TTG	AAT	AAA	AGC	AGG	ACC	ATT	TCC	AGA	TTC	AGT	518
	Arg	Thr	Phe	Met	Val	Leu	Asn	Lys	Ser	Arg	Thr	Ile	Ser	Arg	Phe	Ser	
35	90					95						100			105		
	GCC	ACT	TGG	GCC	CTG	TGG	CTC	TTC	AGT	CCC	TTC	AAC	CTG	ATC	AGA	AGA	566
	Ala	Thr	Trp	Ala	Leu	Trp	Leu	Phe	Ser	Pro	Phe	Asn	Leu	Ile	Arg	Arg	
40	110									115				120			
	ACA	GCC	ATC	AAA	GTG	TCT	GTC	CAT	TCC	TGG	TTC	TCC	ATA	TTC	ATC	ACC	614
	Thr	Ala	Ile	Lys	Val	Ser	Val	His	Ser	Trp	Phe	Ser	Ile	Phe	Ile	Thr	
45	125					130								135			
	ATC	ACT	ATT	TTG	GTC	AAC	TGC	GTG	TGC	ATG	ACC	CGA	ACT	GAT	CTT	CCA	662
	Ile	Thr	Ile	Leu	Val	Asn	Cys	Val	Cys	Met	Thr	Arg	Thr	Asp	Leu	Pro	
50	140					145								150			
	GAG	AAA	GTC	GAG	TAC	GTC	TTC	ACT	GTC	ATT	TAC	ACC	TTC	GAG	GCT	CTG	710
	Glu	Lys	Val	Glu	Tyr	Val	Phe	Thr	Val	Ile	Tyr	Thr	Phe	Glu	Ala	Leu	
55	155					160								165			
	ATT	AAG	ATA	CTG	GCA	AGA	GGG	TTT	TGT	CTA	AAT	GAG	TTC	ACT	TAT	CTT	758
	Ile	Lys	Ile	Leu	Ala	Arg	Gly	Phe	Cys	Leu	Asn	Glu	Phe	Thr	Tyr	Leu	
60	170					175						180			185		
	CGA	GAT	CCG	TGG	AAC	TGG	CTG	GAC	TTC	AGT	GTC	ATT	ACC	TTG	GCG	TAT	806
	Arg	Asp	Pro	Trp	Asn	Trp	Leu	Asp	Phe	Ser	Val	Ile	Thr	Leu	Ala	Tyr	
65	190								195					200			
	GTG	GGT	GCA	GCG	ATA	GAC	CTC	CGA	GGA	ATC	TCA	GGC	CTG	CGG	ACA	TTC	854
	Val	Gly	Ala	Ala	Ile	Asp	Leu	Arg	Gly	Ile	Ser	Gly	Leu	Arg	Thr	Phe	
70	205					210								215			
	CGA	GTT	CTC	AGA	GCC	CTG	AAA	ACT	GTT	TCT	GTG	ATC	CCA	GGA	CTG	AAG	902
	Arg	Val	Leu	Arg	Ala	Leu	Lys	Thr	Val	Ser	Val	Ile	Pro	Gly	Leu	Lys	
75	220					225							230				
	GTC	ATC	GTG	GGA	GCC	CTG	ATC	CAC	TCA	GTG	AGG	AAG	CTG	GCC	GAC	GTG	950
	Val	Ile	Val	Gly	Ala	Leu	Ile	His	Ser	Val	Arg	Lys	Leu	Ala	Asp	Val	
80	235					240						245					

	ACT ATC CTC ACA GTC TTC TGC CTG AGC GTC TTC GCC TTG GTG GGC CTG Thr Ile Leu Thr Val Phe Cys Leu Ser Val Phe Ala Leu Val Gly Leu 250 255 260 265	998
5	CAG CTC TTT AAG GGG AAC CTT AAG AAC AAA TGC ATC AGG AAC GGA ACA Gln Leu Phe Lys Gly Asn Leu Lys Asn Lys Cys Ile Arg Asn Gly Thr 270 275 280	1046
10	GAT CCC CAC AAG GCT GAC AAC CTC TCA TCT GAA ATG GCA GAA TAC GTC Asp Pro His Lys Ala Asp Asn Leu Ser Ser Glu Met Ala Glu Tyr Val 285 290 295	1094
15	TCC ATC AAG CCT GGT ACT ACG GAT CCC TTA CTG TGC GGC AAT GGG TCT Ser Ile Lys Pro Gly Thr Thr Asp Pro Leu Leu Cys Gly Asn Gly Ser 300 305 310	1142
20	GAT GCT GGT CAC TGC CCT GGA GGC TAT GTC TGC CTG AAA ACT CCT GAC Asp Ala Gly His Cys Pro Gly Gly Tyr Val Cys Leu Lys Thr Pro Asp 315 320 325	1190
25	AAC CCG GAT TTT AAC TAC ACC AGC TTT GAT TCC TTT GCG TGG GCA TTC Asn Pro Asp Phe Asn Tyr Thr Ser Phe Asp Ser Phe Ala Trp Ala Phe 330 335 340 345	1238
30	CTC TCA CTG TTC CGC CTC ATG ACG CAG GAC TCC TGG GAG CGC CTG TAC Leu Ser Leu Phe Arg Leu Met Thr Gln Asp Ser Trp Glu Arg Leu Tyr 350 355 360	1286
35	CAG CAG ACA CTC CGG GCT TCT GGG AAA ATG TAC ATG GTC TTT TTC GTG Gln Gln Thr Leu Arg Ala Ser Gly Lys Met Tyr Met Val Phe Phe Val 365 370 375	1334
40	CTG GTT ATT TTC CTT GGA TCG TTC TAC CTG GTC AAT TTG ATC TTG GCC Leu Val Ile Phe Leu Gly Ser Phe Tyr Leu Val Asn Leu Ile Leu Ala 380 385 390	1382
45	GTG GTC ACC ATG GCG TAT GAA GAG CAG AGC CAG GCA ACA ATT GCA GAA Val Val Thr Met Ala Tyr Glu Glu Gln Ser Gln Ala Thr Ile Ala Glu 395 400 405	1430
50	ATC GAA GCC AAG GAA AAA AAG TTC CAG GAA GCC CTT GAG GTG CTG CAG Ile Glu Ala Lys Glu Lys Phe Gln Glu Ala Leu Glu Val Leu Gln 410 415 420 425	1478
55	AAG GAA CAG GAG GTG CTG GCA GCC CTG GGG ATT GAC ACG ACC TCG CTC Lys Glu Gln Glu Val Leu Ala Ala Leu Gly Ile Asp Thr Thr Ser Leu 430 435 440	1526
60	CAG TCC CAC AGT GGA TCA CCC TTA GCC TCC AAA AAC GGC AAT GAG AGA Gln Ser His Ser Gly Ser Pro Leu Ala Ser Lys Asn Ala Asn Glu Arg 445 450 455	1574
65	AGA CCC AGG GTG AAA TCA AGG GTG TCA GAG GGC TCC ACG GAT GAC AAC Arg Pro Arg Val Lys Ser Arg Val Ser Glu Gly Ser Thr Asp Asp Asn 460 465 470	1622
70	AGG TCA CCC CAA TCT GAC CCT TAC AAC CAG CGC AGG ATG TCT TTC CTA Arg Ser Pro Gln Ser Asp Pro Tyr Asn Gln Arg Arg Met Ser Phe Leu 475 480 485	1670
75	GGC CTG TCT TCA GGA AGA CGC AGG GCT AGC CAC GGC AGT GTG TTC CAC Gly Leu Ser Ser Gly Arg Arg Ala Ser His Gly Ser Val Phe His 490 495 500	1718

	TTC CGA GCG CCC AGC CAA GAC ATC TCA TTT CCT GAC GGG ATC ACC CCT Phe Arg Ala Pro Ser Gln Asp Ile Ser Phe Pro Asp Gly Ile Thr Pro 510	515	520	1766
5	GAT GAT GGG GTC TTT CAC GGA GAC CAG GAA AGC CGT CGA GGT TCC ATA Asp Asp Gly Val Phe His Gly Asp Gln Glu Ser Arg Arg Gly Ser Ile 525	530	535	1814
10	TTG CTG GGC AGG GGT GCT GGG CAG ACA GGT CCA CTC CCC AGG AGC CCA Leu Leu Gly Arg Gly Ala Gly Gln Thr Gly Pro Leu Pro Arg Ser Pro 540	545	550	1862
15	CTG CCT CAG TCC CCC AAC CCT GGC CGT AGA CAT GGA GAA GAG GGA CAG Leu Pro Gln Ser Pro Asn Pro Gly Arg Arg His Gly Glu Glu Gly Gln 555	560	565	1910
20	CTC GGA GTG CCC ACT GGT GAG CTT ACC GCT GGA GCG CCT GAA GGC CCG Leu Gly Val Pro Thr Gly Glu Leu Thr Ala Gly Ala Pro Glu Gly Pro 570	575	580	1958
	GCA CTG CAC ACT ACA GGG CAG AAG AGC TTC CTG TCT GCG GGC TAC TTG Ala Leu His Thr Thr Gly Gln Lys Ser Phe Leu Ser Ala Gly Tyr Leu 590	595	600	2006
25	AAC GAA CCT TTC CGA GCA CAG AGG GCC ATG AGC GTT GTC AGT ATC ATG Asn Glu Pro Phe Arg Ala Gln Arg Ala Met Ser Val Val Ser Ile Met 605	610	615	2054
30	ACT TCT GTC ATT GAG GAG CTT GAA GAG TCT AAG CTG AAG TGC CCA CCC Thr Ser Val Ile Glu Glu Leu Glu Ser Lys Leu Lys Cys Pro Pro 620	625	630	2102
35	TGC TTG ATC AGC TTC GCT CAG AAG TAT CTG ATC TGG GAG TGC TGC CCC Cys Leu Ile Ser Phe Ala Gln Lys Tyr Leu Ile Trp Glu Cys Cys Pro 635	640	645	2150
40	AAG TGG AGG AAG TTC AAG ATG GCG CTG TTC GAG CTG GTG ACT GAC CCC Lys Trp Arg Lys Phe Lys Met Ala Leu Phe Glu Leu Val Thr Asp Pro 650	655	660	2198
	TTC GCA GAG CTT ACC ATC ACC CTC TGC ATC GTG GTG AAC ACC GTC TTC Phe Ala Glu Leu Thr Ile Thr Leu Cys Ile Val Val Asn Thr Val Phe 670	675	680	2246
45	ATG GCC ATG GAG CAC TAC CCC ATG ACC GAT GCC TTC GAT GCC ATG CTT Met Ala Met Glu His Tyr Pro Met Thr Asp Ala Phe Asp Ala Met Leu 685	690	695	2294
50	CAA GCC GGC AAC ATT GTC TTC ACC GTG TTT TTC ACA ATG GAG ATG GCC Gln Ala Gly Asn Ile Val Phe Thr Val Phe Phe Thr Met Glu Met Ala 700	705	710	2342
55	TTC AAG ATC ATT GCC TTC GAC CCC TAC TAT TAC TTC CAG AAG AAG TGG Phe Lys Ile Ile Ala Phe Asp Pro Tyr Tyr Tyr Phe Gln Lys Lys Trp 715	720	725	2390
60	AAT ATC TTC GAC TGT GTC ATC GTC ACC GTG AGC CTT CTG GAG CTG AGT Asn Ile Phe Asp Cys Val Ile Val Thr Val Ser Leu Leu Glu Leu Ser 730	735	740	2438
	GCA TCC AAG AAG GGC AGC CTG TCT GTG CTC CGT ACC TTA CGC TTG CTG Ala Ser Lys Lys Gly Ser Leu Ser Val Leu Arg Thr Leu Arg Leu Leu 750	755	760	2486

	CGG GTC TTC AAG CTG GCC AAG TCC TGG CCC ACC CTG AAC ACC CTC ATC Arg Val Phe Lys Leu Ala Lys Ser Trp Pro Thr Leu Asn Thr Leu Ile 765 770 775	2534
5	AAG ATC ATC GGG AAC TCA GTG GGG GCC CTG GGC AAC CTG ACC TTT ATC Lys Ile Ile Gly Asn Ser Val Gly Ala Leu Gly Asn Leu Thr Phe Ile 780 785 790	2582
10	CTG GCC ATC ATC GTC TTC ATC TTC GCC CTG GTC GGA AAG CAG CTT CTC Leu Ala Ile Ile Val Phe Ile Phe Ala Leu Val Gly Lys Gln Leu Leu 795 800 805	2630
15	TCA GAG GAC TAC GGG TGC CGC AAG GAC GGC GTC TCC GTG TGG AAC GGC Ser Glu Asp Tyr Gly Cys Arg Lys Asp Gly Val Ser Val Trp Asn Gly 810 815 820 825	2678
20	GAG AAG CTC CGC TGG CAC ATG TGT GAC TTC TTC CAT TCC TTC CTG GTC Glu Lys Leu Arg Trp His Met Cys Asp Phe Phe His Ser Phe Leu Val 830 835 840	2726
25	GTC TTC CGA ATC CTC TGC GGG GAG TGG ATC GAG AAC ATG TGG GTC TGC Val Phe Arg Ile Leu Cys Gly Glu Trp Ile Glu Asn Met Trp Val Cys 845 850 855	2774
30	ATG GAG GTC AGC CAG AAA TCC ATC TGC CTC ATC CTC TTC TTG ACT GTG Met Glu Val Ser Gln Lys Ser Ile Cys Leu Ile Leu Phe Leu Thr Val 860 865 870	2822
35	ATG GTG CTG GGC AAC CTA GTG GTG CTC AAC CTT TTC ATC GCT TTA CTG Met Val Leu Gly Asn Leu Val Val Leu Asn Leu Phe Ile Ala Leu Leu 875 880 885	2870
40	CTG AAC TCC TTC AGC GCG GAC AAC CTC ACG GCT CCA GAG GAT GAC GGG Leu Asn Ser Phe Ser Ala Asp Asn Leu Thr Ala Pro Glu Asp Asp Gly 890 895 900 905	2918
45	GAG GTG AAC AAC TTG CAG TTA GCA CTG GCC AGG ATC CAG GTA CTT GGC Glu Val Asn Asn Leu Gln Leu Ala Leu Ala Arg Ile Gln Val Leu Gly 910 915 920	2966
50	CAT CGG GCC AGC AGG GCC AGC GGC AGT TAC ATC AGC AGC CAC TGC CGA His Arg Ala Ser Arg Ala Ser Ala Ser Tyr Ile Ser Ser His Cys Arg 925 930 935	3014
55	TTC CAC TGG CCC AAG GTG GAG ACC CAG CTG GGC ATG AAG CCC CCA CTC Phe His Trp Pro Lys Val Glu Thr Gln Leu Gly Met Lys Pro Pro Leu 940 945 950	3062
60	ACC AGC TCA GAG GCC AAG AAC CAC ATT GCC ACT GAT GCT GTC AGT GCT Thr Ser Ser Glu Ala Lys Asn His Ile Ala Thr Asp Ala Val Ser Ala 955 960 965	3110
65	GCA GTG GGG AAC CTG ACA AAG CCA GCT CTC AGT AGC CCC AAG GAG AAC Ala Val Gly Asn Leu Thr Lys Pro Ala Leu Ser Ser Pro Lys Glu Asn 970 975 980 985	3158
70	CAC GGG GAC TTC ATC ACT GAT CCC AAC GTG TGG GTC TCT GTG CCC ATT His Gly Asp Phe Ile Thr Asp Pro Asn Val Trp Val Ser Val Pro Ile 990 995 1000	3206
75	GCT GAG GGG GAA TCT GAC CTC GAC GAG CTC GAG GAA GAT ATG GAG CAG Ala Glu Gly Glu Ser Asp Leu Asp Glu Leu Glu Asp Met Glu Gln 1005 1010 1015	3254

	GCT TCG CAG AGC TCC TGG CAG GAA GAG GAC CCC AAG GGA CAG CAG GAG Ala Ser Gln Ser Ser Trp Gln Glu Glu Asp Pro Lys Gly Gln Gln Glu 1020 1025 1030	3302
5	CAG TTG CCA CAA GTC CAA AAG TGT GAA AAC CAC CAG GCA GCC AGA AGC Gln Leu Pro Gln Val Gln Lys Cys Glu Asn His Gln Ala Ala Arg Ser 1035 1040 1045	3350
10	CCA GCC TCC ATG ATG TCC TCT GAG GAC CTG GCT CCA TAC CTG GGT GAG Pro Ala Ser Met Met Ser Ser Glu Asp Leu Ala Pro Tyr Leu Gly Glu 1050 1055 1060 1065	3398
15	AGC TGG AAG AGG AAG GAT AGC CCT CAG GTC CCT GCC GAG GGA GTG GAT Ser Trp Lys Arg Lys Asp Ser Pro Gln Val Pro Ala Glu Gly Val Asp 1070 1075 1080	3446
20	GAC ACG AGC TCC TCT GAG GGC AGC ACG GTG GAC TGC CCG GAC CCA GAG Asp Thr Ser Ser Glu Gly Ser Thr Val Asp Cys Pro Asp Pro Glu 1085 1090 1095	3494
25	GAA ATC CTG AGG AAG ATC CCC GAG CTG GCA CAT GAC CTG GAC GAG CCC Glu Ile Leu Arg Lys Ile Pro Glu Leu Ala His Asp Leu Asp Glu Pro 1100 1105 1110	3542
30	GAT GAC TGT TTC AGA GAA GGC TGC ACT CGC CGC TGT CCC TGC TGC AAC Asp Asp Cys Phe Arg Glu Gly Cys Thr Arg Arg Cys Pro Cys Cys Asn 1115 1120 1125	3590
35	GTG AAT ACT AGC AAG TCT CCT TGG GCC ACA GGC TGG CAG GTG CGC AAG Val Asn Thr Ser Lys Ser Pro Trp Ala Thr Gly Trp Gln Val Arg Lys 1130 1135 1140 1145	3638
40	ACC TGC TAC CGC ATC GTG GAG CAC AGC TGG TTT GAG AGT TTC ATC ATC Thr Cys Tyr Arg Ile Val Glu His Ser Trp Phe Glu Ser Phe Ile Ile 1150 1155 1160	3686
45	TTC ATG ATC CTG CTC AGC AGT GGA GCG CTG GCC TTT GAG GAT AAC TAC Phe Met Ile Leu Leu Ser Ser Gly Ala Leu Ala Phe Glu Asp Asn Tyr 1165 1170 1175	3734
50	CTG GAA GAG AAA CCC CGA GTG AAG TCC GTG CTG GAG TAC ACT GAC CGA Leu Glu Glu Lys Pro Arg Val Lys Ser Val Leu Glu Tyr Thr Asp Arg 1180 1185 1190	3782
55	GTG TTC ACC TTC ATC TTC GTC TTT GAG ATG CTG CTC AAG TGG GTA GCC Val Phe Thr Phe Ile Phe Val Phe Glu Met Leu Leu Lys Trp Val Ala 1195 1200 1205	3830
60	TAT GGC TTC AAA AAG TAT TTC ACC AAT GCC TGG TGC TGG CTG GAC TTC Tyr Gly Phe Lys Lys Tyr Phe Thr Asn Ala Trp Cys Trp Leu Asp Phe 1210 1215 1220 1225	3878
	CTC ATT GTG AAC ATC TCC CTG ACA AGC CTC ATA GCG AAG ATC CTT GAG Leu Ile Val Asn Ile Ser Leu Thr Ser Leu Ile Ala Lys Ile Leu Glu 1230 1235 1240	3926
	TAT TCC GAC GTG GCG TCC ATC AAA GCC CTT CGG ACT CTC CGT GCC CTC Tyr Ser Asp Val Ala Ser Ile Lys Ala Leu Arg Thr Leu Arg Ala Leu 1245 1250 1255	3974
	CGA CCG CTG CGG GCT CTG TCT CGA TTC GAA GGC ATG AGG GTA GTG GTG Arg Pro Leu Arg Ala Leu Ser Arg Phe Glu Gly Met Arg Val Val Val 1260 1265 1270	4022

	GAT GCC CTC GTG GGC GCC ATC CCC TCC ATC ATG AAC GTC CTC CTC GTC	4070
	Asp Ala Leu Val Gly Ala Ile Pro Ser Ile Met Asn Val Leu Leu Val	
5	1275 1280 1285	
	TGC CTC ATC TTC TGG CTC ATC TTC AGC ATC ATG GGC GTG AAC CTC TTC	4118
	Cys Leu Ile Phe Trp Leu Ile Phe Ser Ile Met Gly Val Asn Leu Phe	
	1290 1295 1300 1305	
10	GCC GGG AAA TTT TCG AAG TGC GTC GAC ACC AGA AAT AAC CCA TTT TCC	4166
	Ala Gly Lys Phe Ser Lys Cys Val Asp Thr Arg Asn Asn Pro Phe Ser	
	1310 1315 1320	
15	AAC GTG AAT TCG ACG ATG GTG AAT AAC AAG TCC GAG TGT CAC AAT CAA	4214
	Asn Val Asn Ser Thr Met Val Asn Asn Lys Ser Glu Cys His Asn Gln	
	1325 1330 1335	
20	AAC AGC ACC GGC CAC TTC TTC TGG GTC AAC GTC AAA GTC AAC TTC GAC	4262
	Asn Ser Thr Gly His Phe Phe Trp Val Asn Val Lys Val Asn Phe Asp	
	1340 1345 1350	
	AAC GTC GCT ATG GGC TAC CTC GCA CTT CTT CAG GTG GCA ACC TTC AAA	4310
	Asn Val Ala Met Gly Tyr Leu Ala Leu Leu Gln Val Ala Thr Phe Lys	
25	1355 1360 1365	
	GGC TGG ATG GAC ATA ATG TAT GCA GCT GTT GAT TCC GGA GAG ATC AAC	4358
	Gly Trp Met Asp Ile Met Tyr Ala Ala Val Asp Ser Gly Glu Ile Asn	
	1370 1375 1380 1385	
30	AGT CAG CCT AAC TGG GAG AAC AAC TTG TAC ATG TAC CTG TAC TTC GTC	4406
	Ser Gln Pro Asn Trp Glu Asn Asn Leu Tyr Met Tyr Leu Tyr Phe Val	
	1390 1395 1400	
35	GTT TTC ATC ATT TTC GGT GGC TTC TTC ACG CTG AAT CTC TTT GTT GGG	4454
	Val Phe Ile Ile Phe Gly Gly Phe Phe Thr Leu Asn Leu Phe Val Gly	
	1405 1410 1415	
40	GTC ATA ATC GAC AAC TTC AAC CAA CAG AAA AAA AAG CTA GGA GGC CAG	4502
	Val Ile Ile Asp Asn Phe Asn Gln Gln Lys Lys Lys Leu Gly Gly Gln	
	1420 1425 1430	
	GAC ATC TTC ATG ACA GAA GAG CAG AAG AAG TAC TAC AAT GCC ATG AAG	4550
	Asp Ile Phe Met Thr Glu Glu Gln Lys Lys Tyr Tyr Asn Ala Met Lys	
45	1435 1440 1445	
	AAG CTG GGC TCC AAG AAA CCC CAG AAG CCC ATC CGA CGG CCC CTG AAT	4598
	Lys Leu Gly Ser Lys Lys Pro Gln Lys Pro Ile Pro Arg Pro Leu Asn	
	1450 1455 1460 1465	
50	AAG TAC CAA GGC TTC GTG TTT GAC ATC GTG ACC AGG CAA GCC TTT GAC	4646
	Lys Tyr Gln Gly Phe Val Phe Asp Ile Val Thr Arg Gln Ala Phe Asp	
	1470 1475 1480	
55	ATC ATC ATC ATG GTT CTC ATC TGC CTC AAC ATG ATC ACC ATG ATG GTG	4694
	Ile Ile Ile Met Val Leu Ile Cys Leu Asn Met Ile Thr Met Met Val	
	1485 1490 1495	
60	GAG ACC GAC GAG CAG GGC GAG GAG AAG ACG AAG GTT CTG GGC AGA ATC	4742
	Glu Thr Asp Glu Gln Gly Glu Glu Lys Thr Lys Val Leu Gly Arg Ile	
	1500 1505 1510	
	AAC CAG TTC TTT GTG GCC GTC TTC ACG GGC GAG TGT GTG ATG AAG ATG	4790
	Asn Gln Phe Phe Val Ala Val Phe Thr Gly Glu Cys Val Met Lys Met	
	1515 1520 1525	

	TTC GCC CTG CGA CAG TAC TAC TTC ACC AAC GGC TGG AAC GTG TTC GAC Phe Ala Leu Arg Gln Tyr Tyr Phe Thr Asn Gly Trp Asn Val Phe Asp 1530 1535 1540 1545	4838
5	TTC ATA GTG GTG ATC CTG TCC ATT GGG AGT CTG CTG TTT TCT GCA ATC Phe Ile Val Val Ile Leu Ser Ile Gly Ser Leu Leu Phe Ser Ala Ile 1550 1555 1560	4886
10	CTT AAG TCA CTG GAA AAC TAC TTC TCC CCG ACG CTC TTC CGG GTC ATC Leu Lys Ser Leu Glu Asn Tyr Phe Ser Pro Thr Leu Phe Arg Val Ile 1565 1570 1575	4934
15	CGT CTG GCC AGG ATC GGC CGC ATC CTC AGG CTG ATC CGA GCA GCC AAG Arg Leu Ala Arg Ile Gly Arg Ile Leu Arg Leu Ile Arg Ala Ala Lys 1580 1585 1590	4982
20	GGG ATT CGC ACG CTG CTC TTC GCC CTC ATG ATG TCC CTG CCC GCC CTC Gly Ile Arg Thr Leu Leu Phe Ala Leu Met Met Ser Leu Pro Ala Leu 1595 1600 1605	5030
25	TTC AAC ATC GGC CTC CTC TTC CTC GTC ATG TTC ATC TAC TCC ATC Phe Asn Ile Gly Leu Leu Phe Leu Val Met Phe Ile Tyr Ser Ile 1610 1615 1620 1625	5078
30	TTC GGC ATG GCC AGC TTC GCT AAC GTC GTG GAC GAG GCC GGC ATC GAC Phe Gly Met Ala Ser Phe Ala Asn Val Val Asp Glu Ala Gly Ile Asp 1630 1635 1640	5126
35	GAC ATG TTC AAC TTC AAG ACC TTT GGC AAC AGC ATG CTG TGC CTG TTC Asp Met Phe Asn Phe Lys Thr Phe Gly Asn Ser Met Leu Cys Leu Phe 1645 1650 1655	5174
40	CAG ATC ACC ACC TCG GCC GGC TGG GAC GGC CTC CTC AGC CCC ATC CTC Gln Ile Thr Thr Ser Ala Gly Trp Asp Gly Leu Leu Ser Pro Ile Leu 1660 1665 1670	5222
45	AAC ACG GGG CCT CCC TAC TGC GAC CCC AAC CTG CCC AAC AGC AAC GGC Asn Thr Gly Pro Pro Tyr Cys Asp Pro Asn Leu Pro Asn Ser Asn Gly 1675 1680 1685	5270
50	TCC CGG GGG AAC TGC GGG AGC CCG GCG GTG GGC ATC ATC TTC TTC ACC Ser Arg Gly Asn Cys Gly Ser Pro Ala Val Gly Ile Ile Phe Phe Thr 1690 1695 1700 1705	5318
55	ACC TAC ATC ATC ATC TCC TTC CTC ATC GTG GTC AAC ATG TAC ATC GCA Thr Tyr Ile Ile Ser Phe Leu Ile Val Val Asn Met Tyr Ile Ala 1710 1715 1720	5366
60	GTG ATT CTG GAG AAC TTC AAC GTA GCC ACC GAG GAG AGC ACG GAG CCC Val Ile Leu Glu Asn Phe Asn Val Ala Thr Glu Glu Ser Thr Glu Pro 1725 1730 1735	5414
	CTG AGC GAG GAC GAC TTC GAC ATG TTC TAT GAG ACC TGG GAG AAG TTC Leu Ser Glu Asp Asp Phe Asp Met Phe Tyr Glu Thr Trp Glu Lys Phe 1740 1745 1750	5462
	GAC CCG GAG GCC ACC CAG TTC ATT GCC TTT TCT GCC CTC TCA GAC TTC Asp Pro Glu Ala Thr Gln Phe Ile Ala Phe Ser Ala Leu Ser Asp Phe 1755 1760 1765	5510
	GCG GAC ACG CTC TCC GGC CCT CTT AGA ATC CCC AAA CCC AAC CAG AAT Ala Asp Thr Leu Ser Gly Pro Leu Arg Ile Pro Lys Pro Asn Gln Asn 1770 1775 1780 1785	5558

	ATA TTA ATC CAG ATG GAC CTG CCG TTG GTC CCC GGG GAT AAG ATC CAC Ile Leu Ile Gln Met Asp Leu Pro Leu Val Pro Gly Asp Lys Ile His 1790 1795 1800	5606
5	TGT CTG GAC ATC CTT TTT GCC TTC ACA AAG AAC GTC TTG GGA GAA TCC Cys Leu Asp Ile Leu Phe Ala Phe Thr Lys Asn Val Leu Gly Glu Ser 1805 1810 1815	5654
10	GGG GAG TTG GAC TCC CTG AAG ACC AAT ATG GAA GAG AAG TTT ATG GCG Gly Glu Leu Asp Ser Leu Lys Thr Asn Met Glu Glu Lys Phe Met Ala 1820 1825 1830	5702
15	ACC AAT CTC TCC AAA GCA TCC TAT GAA CCA ATA GCC ACC ACC CTC CGG Thr Asn Leu Ser Lys Ala Ser Tyr Glu Pro Ile Ala Thr Thr Leu Arg 1835 1840 1845	5750
20	TGG AAG CAG GAA GAC CTC TCA GCC ACA GTC ATT CAA AAG GCC TAC CGG Trp Lys Gln Glu Asp Leu Ser Ala Thr Val Ile Gln Lys Ala Tyr Arg 1850 1855 1860 1865	5798
25	AGC TAC ATG CTG CAC CGC TCC TTG ACA CTC TCC AAC ACC CTG CAT GTG Ser Tyr Met Leu His Arg Ser Leu Thr Leu Ser Asn Thr Leu His Val 1870 1875 1880	5846
30	CCC AGG GCT GAG GAG GAT GGC GTG TCA CTT CCC GGG GAA GGC TAC ATT Pro Arg Ala Glu Glu Asp Gly Val Ser Leu Pro Gly Glu Gly Tyr Ile 1885 1890 1895	5894
35	ACA TTC ATG GCA AAC AGT GGA CTC CCG GAC AAA TCA GAA ACT GCC TCT Thr Phe Met Ala Asn Ser Gly Leu Pro Asp Lys Ser Glu Thr Ala Ser 1900 1905 1910	5942
40	GCT ACG TCT TTC CCG CCA TCC TAT GAC AGT GTC ACC AGG GGC CTG AGT Ala Thr Ser Phe Pro Pro Ser Tyr Asp Ser Val Thr Arg Gly Leu Ser 1915 1920 1925	5990
45	GAC CGG GCC AAC ATT AAC CCA TCT AGC TCA ATG CAA AAT GAA GAT GAG Asp Arg Ala Asn Ile Asn Pro Ser Ser Ser Met Gln Asp Glu Asp Glu 1930 1935 1940 1945	6038
50	GTC GCT GCT AAG GAA GGA AAC AGC CCT GGA CCT CAG TGAAGGCACT Val Ala Ala Lys Glu Gly Asn Ser Pro Gly Pro Gln 1950 1955	6084
55	CAGGCATGCA CAGGGCAGGT TCCAATGTCT TTCTCTGCTG TACTAATCCT TTCCCTCTGG AGGTGGCACCC AACCTCCAGC CTCCACCAAT GCATGTCACT GGTCATGGTG TCAGAACTGA ATGGGGACAT CCTTGAGAAA GCCCCCACCC CAATAGGAAT CAAAGCCAA GGATACTCCT CCATTCTGAC GTCCCTTCCG AGTCCCAGA AGATGTCATT GCTCCCTCT GTTTGTGACC AGAGACGTGA TTCACCAACT TCTCGGAGCC AGAGACACAT AGCAAAGACT TTTCTGCTGG TGTCGGGCAG TCTTAGAGAA GTCACGTAGG GGTTGGTACT GAGAATTAGG GTTGCATGA CTGCATGCTC ACAGCTGCCG GACAATACCT GTGAGTCGGC CATTAAAATT AATATTTTA 60 AAGTTAAAAA AAAAAAA	6144 6204 6264 6324 6384 6444 6504 6524

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
 5 (A) LENGTH: 1957 amino acids
 (B) TYPE: amino acid
 (C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

	Met	Glu	Leu	Pro	Phe	Ala	Ser	Val	Gly	Thr	Thr	Asn	Phe	Arg	Arg	Phe
1					5					10				15		
15	Thr	Pro	Glu	Ser	Leu	Ala	Glu	Ile	Glu	Lys	Gln	Ile	Ala	Ala	His	Arg
					20				25					30		
20	Ala	Ala	Lys	Lys	Ala	Arg	Thr	Lys	His	Arg	Gly	Gln	Glu	Asp	Lys	Gly
			35					40				45				
25	Glu	Lys	Pro	Arg	Pro	Gln	Leu	Asp	Leu	Lys	Asp	Cys	Asn	Gln	Leu	Pro
			50				55				60					
30	Lys	Phe	Tyr	Gly	Glu	Leu	Pro	Ala	Glu	Leu	Val	Gly	Glu	Pro	Leu	Glu
	65				70					75				80		
35	Asp	Leu	Asp	Pro	Phe	Tyr	Ser	Thr	His	Arg	Thr	Phe	Met	Val	Leu	Asn
					85				90					95		
40	Lys	Ser	Arg	Thr	Ile	Ser	Arg	Phe	Ser	Ala	Thr	Trp	Ala	Leu	Trp	Leu
					100				105					110		
45	Phe	Ser	Pro	Phe	Asn	Leu	Ile	Arg	Arg	Thr	Ala	Ile	Lys	Val	Ser	Val
			115				120						125			
50	His	Ser	Trp	Phe	Ser	Ile	Phe	Ile	Thr	Ile	Thr	Ile	Leu	Val	Asn	Cys
						130		135					140			
55	Val	Cys	Met	Thr	Arg	Thr	Asp	Leu	Pro	Glu	Lys	Val	Glu	Tyr	Val	Phe
	145				150					155				160		
60	Thr	Val	Ile	Tyr	Thr	Phe	Glu	Ala	Leu	Ile	Lys	Ile	Leu	Ala	Arg	Gly
					165				170					175		
65	Phe	Cys	Leu	Asn	Glu	Phe	Thr	Tyr	Leu	Arg	Asp	Pro	Trp	Asn	Trp	Leu
					180			185					190			
70	Asp	Phe	Ser	Val	Ile	Thr	Leu	Ala	Tyr	Val	Gly	Ala	Ala	Ile	Asp	Leu
					195			200					205			
75	Arg	Gly	Ile	Ser	Gly	Leu	Arg	Thr	Phe	Arg	Val	Leu	Arg	Ala	Leu	Lys
					210		215					220				
80	Thr	Val	Ser	Val	Ile	Pro	Gly	Leu	Lys	Val	Ile	Val	Gly	Ala	Leu	Ile
	225				230				235				240			
85	His	Ser	Val	Arg	Lys	Leu	Ala	Asp	Val	Thr	Ile	Leu	Thr	Val	Phe	Cys
					245				250				255			
90	Leu	Ser	Val	Phe	Ala	Leu	Val	Gly	Leu	Gln	Leu	Phe	Lys	Gly	Asn	Leu
					260				265				270			
95	Lys	Asn	Lys	Cys	Ile	Arg	Asn	Gly	Thr	Asp	Pro	His	Lys	Ala	Asp	Asn
					275			280				285				

Leu Ser Ser Glu Met Ala Glu Tyr Val Ser Ile Lys Pro Gly Thr Thr
290 295 300

Asp Pro Leu Leu Cys Gly Asn Gly Ser Asp Ala Gly His Cys Pro Gly
305 310 315 320

Gly Tyr Val Cys Leu Lys Thr Pro Asp Asn Pro Asp Phe Asn Tyr Thr
325 330 335

Ser Phe Asp Ser Phe Ala Trp Ala Phe Leu Ser Leu Phe Arg Leu Met
340 345 350

Thr Gln Asp Ser Trp Glu Arg Leu Tyr Gln Gln Thr Leu Arg Ala Ser
355 360 365

Gly Lys Met Tyr Met Val Phe Phe Val Leu Val Ile Phe Leu Gly Ser
370 375 380

Phe Tyr Leu Val Asn Leu Ile Leu Ala Val Val Thr Met Ala Tyr Glu
385 390 395 400

Glu Gln Ser Gln Ala Thr Ile Ala Glu Ile Glu Ala Lys Glu Lys Lys
405 410 415

Phe Gln Glu Ala Leu Glu Val Leu Gln Lys Glu Gln Glu Val Leu Ala
420 425 430

Ala Leu Gly Ile Asp Thr Thr Ser Leu Gln Ser His Ser Gly Ser Pro
435 440 445

Leu Ala Ser Lys Asn Ala Asn Glu Arg Arg Pro Arg Val Lys Ser Arg
450 455 460

Val Ser Glu Gly Ser Thr Asp Asp Asn Arg Ser Pro Gln Ser Asp Pro
465 470 475 480

Tyr Asn Gln Arg Arg Met Ser Phe Leu Gly Leu Ser Ser Gly Arg Arg
485 490 495

Arg Ala Ser His Gly Ser Val Phe His Phe Arg Ala Pro Ser Gln Asp
500 505 510

Ile Ser Phe Pro Asp Gly Ile Thr Pro Asp Asp/Gly Val Phe His Gly
515 520 525

Asp Gln Glu Ser Arg Arg Gly Ser Ile Leu Leu Gly Arg Gly Ala Gly
530 535 540

Gln Thr Gly Pro Leu Pro Arg Ser Pro Leu Pro Gln Ser Pro Asn Pro
545 550 555 560

Gly Arg Arg His Gly Glu Glu Gly Gln Leu Gly Val Pro Thr Gly Glu
565 570 575

Leu Thr Ala Gly Ala Pro Glu Gly Pro Ala Leu His Thr Thr Gly Gln
580 585 590

Lys Ser Phe Leu Ser Ala Gly Tyr Leu Asn Glu Pro Phe Arg Ala Gln
595 600 605

Arg Ala Met Ser Val Val Ser Ile Met Thr Ser Val Ile Glu Glu Leu
610 615 620

Glu Glu Ser Lys Leu Lys Cys Pro Pro Cys Leu Ile Ser Phe Ala Gln
 625 630 635 640

5 Lys Tyr Leu Ile Trp Glu Cys Cys Pro Lys Trp Arg Lys Phe Lys Met
 645 650 655

Ala Leu Phe Glu Leu Val Thr Asp Pro Phe Ala Glu Leu Thr Ile Thr
 660 665 670

10 Leu Cys Ile Val Val Asn Thr Val Phe Met Ala Met Glu His Tyr Pro
 675 680 685

Met Thr Asp Ala Phe Asp Ala Met Leu Gln Ala Gly Asn Ile Val Phe
 690 695 700

15 Thr Val Phe Phe Thr Met Glu Met Ala Phe Lys Ile Ile Ala Phe Asp
 705 710 715 720

20 Pro Tyr Tyr Tyr Phe Gln Lys Lys Trp Asn Ile Phe Asp Cys Val Ile
 725 730 735

Val Thr Val Ser Leu Leu Glu Leu Ser Ala Ser Lys Lys Gly Ser Leu
 740 745 750

25 Ser Val Leu Arg Thr Leu Arg Leu Leu Arg Val Phe Lys Leu Ala Lys
 755 760 765

Ser Trp Pro Thr Leu Asn Thr Leu Ile Lys Ile Ile Gly Asn Ser Val
 770 775 780

30 Gly Ala Leu Gly Asn Leu Thr Phe Ile Leu Ala Ile Ile Val Phe Ile
 785 790 795 800

35 Phe Ala Leu Val Gly Lys Gln Leu Leu Ser Glu Asp Tyr Gly Cys Arg
 805 810 815

Lys Asp Gly Val Ser Val Trp Asn Gly Glu Lys Leu Arg Trp His Met
 820 825 830

40 Cys Asp Phe Phe His Ser Phe Leu Val Val Phe Arg Ile Leu Cys Gly
 835 840 845

Glu Trp Ile Glu Asn Met Trp Val Cys Met Glu Val Ser Gln Lys Ser
 850 855 860

45 Ile Cys Leu Ile Leu Phe Leu Thr Val Met Val Leu Gly Asn Leu Val
 865 870 875 880

50 Val Leu Asn Leu Phe Ile Ala Leu Leu Leu Asn Ser Phe Ser Ala Asp
 885 890 895

Asn Leu Thr Ala Pro Glu Asp Asp Gly Glu Val Asn Asn Leu Gln Leu
 900 905 910

55 Ala Leu Ala Arg Ile Gln Val Leu Gly His Arg Ala Ser Arg Ala Ser
 915 920 925

60 Ala Ser Tyr Ile Ser Ser His Cys Arg Phe His Trp Pro Lys Val Glu
 930 935 940

Thr Gln Leu Gly Met Lys Pro Pro Leu Thr Ser Ser Glu Ala Lys Asn
 945 950 955 960

His Ile Ala Thr Asp Ala Val Ser Ala Ala Val Gly Asn Leu Thr Lys
 965 970 975

Pro Ala Leu Ser Ser Pro Lys Glu Asn His Gly Asp Phe Ile Thr Asp
 5 980 985 990

Pro Asn Val Trp Val Ser Val Pro Ile Ala Glu Gly Glu Ser Asp Leu
 995 1000 1005

10 Asp Glu Leu Glu Glu Asp Met Glu Gln Ala Ser Gln Ser Ser Trp Gln
 1010 1015 1020

Glu Glu Asp Pro Lys Gly Gln Gln Glu Gln Leu Pro Gln Val Gln Lys
 1025 1030 1035 1040

15 Cys Glu Asn His Gln Ala Ala Arg Ser Pro Ala Ser Met Met Ser Ser
 1045 1050 1055

Glu Asp Leu Ala Pro Tyr Leu Gly Glu Ser Trp Lys Arg Lys Asp Ser
 20 1060 1065 1070

Pro Gln Val Pro Ala Glu Gly Val Asp Asp Thr Ser Ser Glu Gly
 1075 1080 1085

25 Ser Thr Val Asp Cys Pro Asp Pro Glu Glu Ile Leu Arg Lys Ile Pro
 1090 1095 1100

Glu Leu Ala His Asp Leu Asp Glu Pro Asp Asp Cys Phe Arg Glu Gly
 30 1105 1110 1115 1120

Cys Thr Arg Arg Cys Pro Cys Cys Asn Val Asn Thr Ser Lys Ser Pro
 1125 1130 1135

Trp Ala Thr Gly Trp Gln Val Arg Lys Thr Cys Tyr Arg Ile Val Glu
 35 1140 1145 1150

His Ser Trp Phe Glu Ser Phe Ile Ile Phe Met Ile Leu Leu Ser Ser
 40 1155 1160 1165

Gly Ala Leu Ala Phe Glu Asp Asn Tyr Leu Glu Glu Lys Pro Arg Val
 1170 1175 1180

Lys Ser Val Leu Glu Tyr Thr Asp Arg Val Phe Thr Phe Ile Phe Val
 45 1185 1190 1195 1200

Phe Glu Met Leu Leu Lys Trp Val Ala Tyr Gly Phe Lys Lys Tyr Phe
 50 1205 1210 1215

Thr Asn Ala Trp Cys Trp Leu Asp Phe Leu Ile Val Asn Ile Ser Leu
 1220 1225 1230

Thr Ser Leu Ile Ala Lys Ile Leu Glu Tyr Ser Asp Val Ala Ser Ile
 55 1235 1240 1245

Lys Ala Leu Arg Thr Leu Arg Ala Leu Arg Pro Leu Arg Ala Leu Ser
 1250 1255 1260

Arg Phe Glu Gly Met Arg Val Val Val Asp Ala Leu Val Gly Ala Ile
 60 1265 1270 1275 1280

Pro Ser Ile Met Asn Val Leu Leu Val Cys Leu Ile Phe Trp Leu Ile
 1285 1290 1295

Phe Ser Ile Met Gly Val Asn Leu Phe Ala Gly Lys Phe Ser Lys Cys
 65 1300 1305 1310

Val Asp Thr Arg Asn Asn Pro Phe Ser Asn Val Asn Ser Thr Met Val
 1315 1320 1325

5 Asn Asn Lys Ser Glu Cys His Asn Gln Asn Ser Thr Gly His Phe Phe
 1330 1335 1340

Trp Val Asn Val Lys Val Asn Phe Asp Asn Val Ala Met Gly Tyr Leu
 1345 1350 1355 1360

10 Ala Leu Leu Gln Val Ala Thr Phe Lys Gly Trp Met Asp Ile Met Tyr
 1365 1370 1375

Ala Ala Val Asp Ser Gly Glu Ile Asn Ser Gln Pro Asn Trp Glu Asn
 1380 1385 1390

Asn Leu Tyr Met Tyr Leu Tyr Phe Val Val Phe Ile Ile Phe Gly Gly
 1395 1400 1405

20 Phe Phe Thr Leu Asn Leu Phe Val Gly Val Ile Ile Asp Asn Phe Asn
 1410 1415 1420

Gln Gln Lys Lys Lys Leu Gly Gly Gln Asp Ile Phe Met Thr Glu Glu
 1425 1430 1435 1440

25 Gln Lys Lys Tyr Tyr Asn Ala Met Lys Lys Leu Gly Ser Lys Lys Pro
 1445 1450 1455

Gln Lys Pro Ile Pro Arg Pro Leu Asn Lys Tyr Gln Gly Phe Val Phe
 30 1460 1465 1470

Asp Ile Val Thr Arg Gln Ala Phe Asp Ile Ile Ile Met Val Leu Ile
 1475 1480 1485

35 Cys Leu Asn Met Ile Thr Met Met Val Glu Thr Asp Glu Gln Gly Glu
 1490 1495 1500

Glu Lys Thr Lys Val Leu Gly Arg Ile Asn Gln Phe Phe Val Ala Val
 1505 1510 1515 1520

40 Phe Thr Gly Glu Cys Val Met Lys Met Phe Ala Leu Arg Gln Tyr Tyr
 1525 1530 1535

45 Phe Thr Asn Gly Trp Asn Val Phe Asp Phe Ile Val Val Ile Leu Ser
 1540 1545 1550

Ile Gly Ser Leu Leu Phe Ser Ala Ile Leu Lys Ser Leu Glu Asn Tyr
 1555 1560 1565

50 Phe Ser Pro Thr Leu Phe Arg Val Ile Arg Leu Ala Arg Ile Gly Arg
 1570 1575 1580

Ile Leu Arg Leu Ile Arg Ala Ala Lys Gly Ile Arg Thr Leu Leu Phe
 55 1585 1590 1595 1600

Ala Leu Met Met Ser Leu Pro Ala Leu Phe Asn Ile Gly Leu Leu Leu
 1605 1610 1615

Phe Leu Val Met Phe Ile Tyr Ser Ile Phe Gly Met Ala Ser Phe Ala
 60 1620 1625 1630

Asn Val Val Asp Glu Ala Gly Ile Asp Asp Met Phe Asn Phe Lys Thr
 1635 1640 1645

70086

-64-

Phe Gly Asn Ser Met Leu Cys Leu Phe Gln Ile Thr Thr Ser Ala Gly
1650 1655 1660

Trp Asp Gly Leu Leu Ser Pro Ile Leu Asn Thr Gly Pro Pro Tyr Cys
5 1665 1670 1675 1680

Asp Pro Asn Leu Pro Asn Ser Asn Gly Ser Arg Gly Asn Cys Gly Ser
1685 1690 1695

10 Pro Ala Val Gly Ile Ile Phe Phe Thr Thr Tyr Ile Ile Ile Ser Phe
1700 1705 1710

Leu Ile Val Val Asn Met Tyr Ile Ala Val Ile Leu Glu Asn Phe Asn
1715 1720 1725

15 Val Ala Thr Glu Glu Ser Thr Glu Pro Leu Ser Glu Asp Asp Phe Asp
1730 1735 1740

Met Phe Tyr Glu Thr Trp Glu Lys Phe Asp Pro Glu Ala Thr Gln Phe
20 1745 1750 1755 1760

Ile Ala Phe Ser Ala Leu Ser Asp Phe Ala Asp Thr Leu Ser Gly Pro
25 1765 1770 1775

Leu Arg Ile Pro Lys Pro Asn Gln Asn Ile Leu Ile Gln Met Asp Leu
1780 1785 1790

Pro Leu Val Pro Gly Asp Lys Ile His Cys Leu Asp Ile Leu Phe Ala
30 1795 1800 1805

Phe Thr Lys Asn Val Leu Gly Glu Ser Gly Glu Leu Asp Ser Leu Lys
35 1810 1815 1820

Thr Asn Met Glu Glu Lys Phe Met Ala Thr Asn Leu Ser Lys Ala Ser
1825 1830 1835 1840

Tyr Glu Pro Ile Ala Thr Thr Leu Arg Trp Lys Gln Glu Asp Leu Ser
40 1845 1850 1855

Ala Thr Val Ile Gln Lys Ala Tyr Arg Ser Tyr Met Leu His Arg Ser
1860 1865 1870

Leu Thr Leu Ser Asn Thr Leu His Val Pro Arg Ala Glu Glu Asp Gly
45 1875 1880 1885

Val Ser Leu Pro Gly Glu Gly Tyr Ile Thr Phe Met Ala Asn Ser Gly
1890 1895 1900

Leu Pro Asp Lys Ser Glu Thr Ala Ser Ala Thr Ser Phe Pro Pro Ser
50 1905 1910 1915 1920

Tyr Asp Ser Val Thr Arg Gly Leu Ser Asp Arg Ala Asn Ile Asn Pro
55 1925 1930 1935

Ser Ser Ser Met Gln Asn Glu Asp Glu Val Ala Ala Lys Glu Gly Asn
1940 1945 1950

Ser Pro Gly Pro Gln
60 1955

	GTG TTC GAC TTC ATA GTG GTG ATC CTG TCC ATT GGG AGT CTG CTG TTT Val Phe Asp Phe Ile Val Val Ile Leu Ser Ile Gly Ser Leu Leu Phe 110 115 120	926
5	TCT GCA ATC CTT AAG TCA CTG GAA AAC TAC TTC TCC CCG ACG CTC TTC Ser Ala Ile Leu Lys Ser Leu Glu Asn Tyr Phe Ser Pro Thr Leu Phe 125 130 135	974
10	CGG GTC ATC CGT CTG GCC AGG ATC GGC CGC ATC CTC AGG CTG ATC CGA Arg Val Ile Arg Leu Ala Arg Ile Gly Arg Ile Leu Arg Leu Ile Arg 140 145 150	1022
15	GCA GCC AAG GGG ATT CGC ACG CTG CTC TTC GCC CTC ATG ATG TCC CTG Ala Ala Lys Gly Ile Arg Thr Leu Leu Phe Ala Leu Met Met Ser Leu 155 160 165 170	1070
20	CCC GCC CTC TTC AAC ATC GGC CTC CTC TTC CTC GTC ATG TTC ATC Pro Ala Leu Phe Asn Ile Gly Leu Leu Phe Leu Val Met Phe Ile 175 180 185	1118
25	TAC TCC ATC TTC GGC ATG GCC AGC TTC GCT AAC GTC GTG GAC GAG GCC Tyr Ser Ile Phe Gly Met Ala Ser Phe Ala Asn Val Val Asp Glu Ala 190 195 200	1166
30	GGC ATC GAC GAC ATG TTC AAC TTC AAG ACC TTT GGC AAC AGC ATG CTG Gly Ile Asp Asp Met Phe Asn Phe Lys Thr Phe Gly Asn Ser Met Leu 205 210 215	1214
35	TGC CTG TTC CAG ATC ACC ACC TCG GCC GGC TGG GAC GGC CTC CTC AGC Cys Leu Phe Gln Ile Thr Ser Ala Gly Trp Asp Gly Leu Leu Ser 220 225 230	1262
40	CCC ATC CTC AAC ACG GGG CCT CCC TAC TGC GAC CCC AAC CTG CCC AAC Pro Ile Leu Asn Thr Gly Pro Pro Tyr Cys Asp Pro Asn Leu Pro Asn 235 240 245 250	1310
45	AGC AAC GGC TCC CGG GGG AAC TGC GGG AGC CCG GCG GTG GGC ATC ATC Ser Asn Gly Ser Arg Gly Asn Cys Gly Ser Pro Ala Val Gly Ile Ile 255 260 265	1358
50	TTC TTC ACC ACC TAC ATC ATC ATC TCC TTC CTC ATC GTG GTC AAC ATG Phe Phe Thr Thr Tyr Ile Ile Ile Ser Phe Leu Ile Val Val Asn Met 270 275 280	1406
55	TAC ATC GCA GTG ATT CTG GAG AAC TTC AAC GTA GCC ACC GAG GAG AGC Tyr Ile Ala Val Ile Leu Glu Asn Phe Asn Val Ala Thr Glu Glu Ser 285 290 295	1454
60	ACG GAG CCC CTG AGC GAG GAC GAC TTC GAC ATG TTC TAT GAG ACC TGG Thr Glu Pro Leu Ser Glu Asp Asp Phe Asp Met Phe Tyr Glu Thr Trp 300 305 310	1502
65	GAG AAG TTC GAC CCG GAG GCC ACC CAG TTC ATT GCC TTT TCT GCC CTC Glu Lys Phe Asp Pro Glu Ala Thr Gln Phe Ile Ala Phe Ser Ala Leu 315 320 325 330	1550
70	TCA GAC TTC GCG GAC ACG CTC TCC GGC CCT CTT AGA ATC CCC AAA CCC Ser Asp Phe Ala Asp Thr Leu Ser Gly Pro Leu Arg Ile Pro Lys Pro 335 340 345	1598
75	AAC CAG AAT ATA TTA ATC CAG ATG GAC CTG CCG TTG GTC CCC GGG GAT Asn Gln Asn Ile Leu Ile Gln Met Asp Leu Pro Leu Val Pro Gly Asp 350 355 360	1646

	AAG ATC CAC TGT CTG GAC ATC CTT TTT GCC TTC ACA AAG AAC GTC TTG Lys Ile His Cys Leu Asp Ile Leu Phe Ala Phe Thr Lys Asn Val Leu 365 370 375	1694
5	GGA GAA TCC GGG GAG TTG GAC TCC CTG AAG ACC AAT ATG GAA GAG AAG Gly Glu Ser Gly Glu Leu Asp Ser Leu Lys Thr Asn Met Glu Glu Lys 380 385 390	1742
10	TTT ATG GCG ACC AAT CTC TCC AAA GCA TCC TAT GAA CCA ATA GCC ACC Phe Met Ala Thr Asn Leu Ser Lys Ala Ser Tyr Glu Pro Ile Ala Thr 395 400 405 410	1790
15	ACC CTC CGG TGG AAG CAG GAA GAC CTC TCA GCC ACA GTC ATT CAA AAG Thr Leu Arg Trp Lys Gln Glu Asp Leu Ser Ala Thr Val Ile Gln Lys 415 420 425	1838
20	GCC TAC CGG AGC TAC ATG CTG CAC CGC TCC TTG ACA CTC TCC AAC ACC Ala Tyr Arg Ser Tyr Met Leu His Arg Ser Leu Thr Leu Ser Asn Thr 430 435 440	1886
25	CTG CAT GTG CCC AGG GCT GAG GAG GAT GGC GTG TCA CTT CCC GGG GAA Leu His Val Pro Arg Ala Glu Glu Asp Gly Val Ser Leu Pro Gly Glu 445 450 455	1934
30	GGC TAC ATT ACA TTC ATG GCA AAC AGT GGA CTC CCG GAC AAA TCA GAA Gly Tyr Ile Thr Phe Met Ala Asn Ser Gly Leu Pro Asp Lys Ser Glu 460 465 470	1982
35	ACT GCC TCT GCT ACG TCT TTC CCG GCA TCC TAT GAC AGT GTC ACC AGG Thr Ala Ser Ala Thr Ser Phe Pro Pro Ser Tyr Asp Ser Val Thr Arg 475 480 485 490	2030
40	GGC CTG AGT GAC CGG GCC AAC ATT AAC CCA TCT AGC TCA ATG CAA AAT Gly Leu Ser Asp Arg Ala Asn Ile Asn Pro Ser Ser Ser Met Gln Asn 495 500 505	2078
45	GAA GAT GAG GTC GCT GCT AAG GAA GGA AAC AGC CCT GGA CCT CAG TGAAGGCAC Glu Asp Glu Val Ala Ala Lys Glu Gly Asn Ser Pro Gly Pro Gln 510 515 520	2133
50	CAGGCATGCA CAGGGCAGGT TCCAATGTCT TTCTGTGCTG TACTAATCCT TTCCCTCTGG AGGTGGCACCC AACCTCCAGC CTCCACCAAT GCATGTCACT GGTATGGTG TCAGAACTGA ATGGGGACAT CCTTGAGAAA GCCCCCACCC CAATAGGAAT CAAAAGCCAA GGATACTCCT CCATTCTGAC GTCCCTTCCG AGTCCCAGA AGATGTCATT GCTCCCTTCT GTTTGTGACC AGAGACGTGA TTCACCAACT TCTCGGAGCC AGAGACACAT AGCAAAGACT TTTCTGCTGG TGTCGGGCAG TCTTAGAGAA GTCACGTAGG GGTTGGTACT GAGAATTAGG GTTTGCATGA CTGCATGCTC ACAGCTGCCG GACAATACCT GTGAGTCGGC CATTAAAATT AATATTTTA AAGTTAAAAA AAAAAAA	2193 2253 2313 2373 2433 2493 2553 2573

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
5 (A) LENGTH: 521 amino acids
(B) TYPE: amino acid
(C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Thr Glu Glu Gln Lys Lys Tyr Tyr Asn Ala Met Lys Lys Leu Gly
1 5 10 15
Ser Lys Lys Pro Gln Lys Pro Ile Pro Arg Pro Leu Asn Lys Tyr Gln
15 20 25 30
Gly Phe Val Phe Asp Ile Val Thr Arg Gln Ala Phe Asp Ile Ile Ile
20 35 40 45
Met Val Leu Ile Cys Leu Asn Met Ile Thr Met Met Val Glu Thr Asp
25 50 55 60
Glu Gln Gly Glu Glu Lys Thr Lys Val Leu Gly Arg Ile Asn Gln Phe
25 65 70 75 80
Phe Val Ala Val Phe Thr Gly Glu Cys Val Met Lys Met Phe Ala Leu
30 85 90 95
Arg Gln Tyr Tyr Phe Thr Asn Gly Trp Asn Val Phe Asp Phe Ile Val
35 100 105 110
Val Ile Leu Ser Ile Gly Ser Leu Leu Phe Ser Ala Ile Leu Lys Ser
40 115 120 125
Leu Glu Asn Tyr Phe Ser Pro Thr Leu Phe Arg Val Ile Arg Leu Ala
45 130 135 140
Arg Ile Gly Arg Ile Leu Arg Leu Ile Arg Ala Ala Lys Gly Ile Arg
50 145 150 155 160
Thr Leu Leu Phe Ala Leu Met Met Ser Leu Pro Ala Leu Phe Asn Ile
55 165 170 175
Gly Leu Leu Leu Phe Leu Val Met Phe Ile Tyr Ser Ile Phe Gly Met
60 180 185 190
Ala Ser Phe Ala Asn Val Val Asp Glu Ala Gly Ile Asp Asp Met Phe
65 195 200 205
Asn Phe Lys Thr Phe Gly Asn Ser Met Leu Cys Leu Phe Gln Ile Thr
70 210 215 220
Thr Ser Ala Gly Trp Asp Gly Leu Leu Ser Pro Ile Leu Asn Thr Gly
75 225 230 235 240
Pro Pro Tyr Cys Asp Pro Asn Leu Pro Asn Ser Asn Gly Ser Arg Gly
80 245 250 255
Asn Cys Gly Ser Pro Ala Val Gly Ile Ile Phe Phe Thr Thr Tyr Ile
85 260 265 270
Ile Ile Ser Phe Leu Ile Val Val Asn Met Tyr Ile Ala Val Ile Leu
90 275 280 285

Glu Asn Phe Asn Val Ala Thr Glu Glu Ser Thr Glu Pro Leu Ser Glu
 290 295 300

5 Asp Asp Phe Asp Met Phe Tyr Glu Thr Trp Glu Lys Phe Asp Pro Glu
 305 310 315 320

Ala Thr Gln Phe Ile Ala Phe Ser Ala Leu Ser Asp Phe Ala Asp Thr
 325 330 335

10 Leu Ser Gly Pro Leu Arg Ile Pro Lys Pro Asn Gln Asn Ile Leu Ile
 340 345 350

15 Gln Met Asp Leu Pro Leu Val Pro Gly Asp Lys Ile His Cys Leu Asp
 355 360 365

Ile Leu Phe Ala Phe Thr Lys Asn Val Leu Gly Glu Ser Gly Glu Leu
 370 375 380

20 Asp Ser Leu Lys Thr Asn Met Glu Glu Lys Phe Met Ala Thr Asn Leu
 385 390 395 400

Ser Lys Ala Ser Tyr Glu Pro Ile Ala Thr Thr Leu Arg Trp Lys Gln
 405 410 415

25 Glu Asp Leu Ser Ala Thr Val Ile Gln Lys Ala Tyr Arg Ser Tyr Met
 420 425 430

30 Leu His Arg Ser Leu Thr Leu Ser Asn Thr Leu His Val Pro Arg Ala
 435 440 445

Glu Glu Asp Gly Val Ser Leu Pro Gly Glu Gly Tyr Ile Thr Phe Met
 450 455 460

35 Ala Asn Ser Gly Leu Pro Asp Lys Ser Glu Thr Ala Ser Ala Thr Ser
 465 470 475 480

Phe Pro Pro Ser Tyr Asp Ser Val Thr Arg Gly Leu Ser Asp Arg Ala
 485 490 495

40 Asn Ile Asn Pro Ser Ser Ser Met Gln Asn Glu Asp Glu Val Ala Ala
 500 505 510

45 Lys Glu Gly Asn Ser Pro Gly Pro Gln
 515 520

(2) INFORMATION FOR SEQ ID NO:5:

- 50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 7052 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- 55 (ii) MOLECULE TYPE: cDNA
- 60 (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 204..6602

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

	TAGCTTGCTT CTGCTAATGC TACCCCAGGC CTTTAGACAG AGAACAGATG GCAGATGGAG	60
5	TTTCTTATTG CCATGCGCAA ACGCTGAGCC CACCTCATGA TCCCGGACCC CATGGTTTC	120
	AGTAGACAAC CTGGGCTAAG AAGAGATCTC CGACCTTATA GAGCAGCAAA GAGTGTAAAT	180
	TCTTCCCCAA GAAGAATGAG AAG ATG GAG CTC CCC TTT GCG TCC GTG GGA Met Glu Leu Pro Phe Ala Ser Val Gly	230
10	1 5	
	ACT ACC AAT TTC AGA CGG TTC ACT CCA GAG TCA CTG GCA GAG ATC GAG Thr Thr Asn Phe Arg Arg Phe Thr Pro Glu Ser Leu Ala Glu Ile Glu	278
	10 15 20 25	
15	AAG CAG ATT GCT GCT CAC CGG GCA GCC AAG AAG GCC AGA ACC AAG CAC Lys Gln Ile Ala Ala His Arg Ala Ala Lys Lys Ala Arg Thr Lys His	326
	30 35 40	
20	AGA GGA CAG GAG GAC AAG GGC GAG AAG CCC AGG CCT CAG CTG GAC TTG Arg Gly Gln Glu Asp Lys Gly Glu Lys Pro Arg Pro Gln Leu Asp Leu	374
	45 50 55	
25	AAA GAC TGT AAC CAG CTG CCC AAG TTC TAT GGT GAG CTC CCA GCA GAA Lys Asp Cys Asn Gln Leu Pro Lys Phe Tyr Gly Glu Leu Pro Ala Glu	422
	60 65 70	
30	CTG GTC GGG GAG CCC CTG GAG GAC CTA GAC CCT TTC TAC AGC ACA CAC Leu Val Gly Glu Pro Leu Glu Asp Leu Asp Pro Phe Tyr Ser Thr His	470
	75 80 85	
	CGG ACA TTC ATG GTG TTG AAT AAA AGC AGG ACC ATT TCC AGA TTC AGT Arg Thr Phe Met Val Leu Asn Lys Ser Arg Thr Ile Ser Arg Phe Ser	518
	90 95 100 105	
35	GCC ACT TGG GCC CTG TGG CTC TTC AGT CCC TTC AAC CTG ATC AGA AGA Ala Thr Trp Ala Leu Trp Leu Phe Ser Pro Phe Asn Leu Ile Arg Arg	566
	110 115 120	
40	ACA GCC ATC AAA GTG TCT GTC CAT TCC TGG TTC TCC ATA TTC ATC ACC Thr Ala Ile Lys Val Ser Val His Ser Trp Phe Ser Ile Phe Ile Thr	614
	125 130 135	
45	ATC ACT ATT TTG GTC AAC TGC GTG TGC ATG ACC CGA ACT GAT CTT CCA Ile Thr Ile Leu Val Asn Cys Val Cys Met Thr Arg Thr Asp Leu Pro	662
	140 145 150	
50	GAG AAA GTC GAG TAC GTC TTC ACT GTC ATT TAC ACC TTC GAG GCT CTG Glu Lys Val Glu Tyr Val Phe Thr Val Ile Tyr Thr Phe Glu Ala Leu	710
	155 160 165	
	ATT AAG ATA CTG GCA AGA GGG TTT TGT CTA AAT GAG TTC ACT TAT CTT Ile Lys Ile Leu Ala Arg Gly Phe Cys Leu Asn Glu Phe Thr Tyr Leu	758
	170 175 180 185	
55	CGA GAT CCG TGG AAC TGG CTG GAC TTC AGT GTC ATT ACC TTG GCG TAT Arg Asp Pro Trp Asn Trp Leu Asp Phe Ser Val Ile Thr Leu Ala Tyr	806
	190 195 200	
60	190 195 200	
	GTG GGT GCA GCG ATA GAC CTC CGA GGA ATC TCA GGC CTG CGG ACA TTC Val Gly Ala Ala Ile Asp Leu Arg Gly Ile Ser Gly Leu Arg Thr Phe	854
	205 210 215	

CGA	GTT	CTC	AGA	GCC	CTG	AAA	ACT	GTT	TCT	GTG	ATC	CCA	GGA	CTG	AAG	902	
Arg	Val	Leu	Arg	Ala	Leu	Lys	Thr	Val	Ser	Val	Ile	Pro	Gly	Leu	Lys		
220							225				230						
5	GTC	ATC	GTC	GGA	GCC	CTG	ATC	CAC	TCA	GTG	AGG	AAG	CTG	GCC	GAC	GTG	950
	Val	Ile	Val	Gly	Ala	Leu	Ile	His	Ser	Val	Arg	Lys	Leu	Ala	Asp	Val	
	235						240				245						
10	ACT	ATC	CTC	ACA	GTC	TTC	TGC	CTG	AGC	GTC	TTC	GCC	TTG	GTG	GGC	CTG	998
	Thr	Ile	Leu	Thr	Val	Phe	Cys	Leu	Ser	Val	Phe	Ala	Leu	Val	Gly	Leu	
	250					255				260		265					
15	CAG	CTC	TTT	AAG	GGG	AAC	CTT	AAG	AAC	AAA	TGC	ATC	AGG	AAC	GGA	ACA	1046
	Gln	Leu	Phe	Lys	Gly	Asn	Leu	Lys	Asn	Lys	Cys	Ile	Arg	Asn	Gly	Thr	
	270					275					280						
20	GAT	CCC	CAC	AAG	GCT	GAC	AAC	CTC	TCA	TCT	GAA	ATG	GCA	GAA	TAC	ATC	1094
	Asp	Pro	His	Lys	Ala	Asp	Asn	Leu	Ser	Ser	Glu	Met	Ala	Glu	Tyr	Ile	
	285					290					295						
25	TTC	ATC	AAG	CCT	GGT	ACT	ACG	GAT	CCC	TTA	CTG	TGC	GGC	AAT	GGG	TCT	1142
	Phe	Ile	Lys	Pro	Gly	Thr	Asp	Pro	Leu	Leu	Cys	Gly	Asn	Gly	Ser		
	300					305					310						
30	GAT	GCT	GGT	CAC	TGC	CCT	CGA	GGC	TAT	GTC	TGC	CTG	AAA	ACT	CCT	GAC	1190
	Asp	Ala	Gly	His	Cys	Pro	Gly	Gly	Tyr	Val	Cys	Leu	Lys	Thr	Pro	Asp	
	315					320					325						
35	AAC	CCG	GAT	TTT	AAC	TAC	ACC	AGC	TTT	GAT	TCC	TTT	GCG	TGG	GCA	TTC	1238
	Asn	Pro	Asp	Phe	Asn	Tyr	Thr	Ser	Phe	Asp	Ser	Phe	Ala	Trp	Ala	Phe	
	330					335					340				345		
40	CTC	TCA	CTG	TTC	CGC	CTC	ATG	ACG	CAG	GAC	TCC	TGG	GAG	CGC	CTG	TAC	1286
	Leu	Ser	Leu	Phe	Arg	Leu	Met	Thr	Gln	Asp	Ser	Trp	Glu	Arg	Leu	Tyr	
	350					355						360					
45	CAG	CAG	ACA	CTC	CGG	GCT	TCT	GGG	AAA	ATG	TAC	ATG	GTC	TTT	TTC	GTG	1334
	Gln	Gln	Thr	Leu	Arg	Ala	Ser	Gly	Lys	Met	Tyr	Met	Val	Phe	Phe	Val	
	365					370						375					
50	CTG	GTT	ATT	TTC	CTT	GGA	TCG	TTC	TAC	CTG	GTC	AAT	TTG	ATC	TTG	GCC	1382
	Leu	Val	Ile	Phe	Leu	Gly	Ser	Phe	Tyr	Leu	Val	Asn	Ile	Ile	Leu	Ala	
	380					385						390					
55	ATC	GAA	GCC	AAG	GAA	AAA	AAG	TTC	CAG	GAA	GCC	CTT	GAG	GTG	CTG	CAG	1478
	Ile	Glu	Ala	Lys	Glu	Lys	Lys	Phe	Gln	Glu	Ala	Leu	Glu	Val	Leu	Gln	
	410					415					420				425		
60	AAG	GAA	CAG	GAG	GTG	CTG	GCA	GCC	CTG	GGG	ATT	GAC	ACG	ACC	TCG	CTC	1526
	Lys	Glu	Gln	Glu	Val	Leu	Ala	Leu	Gly	Ile	Asp	Thr	Thr	Ser	Leu		
	430					435						440					
	CAG	TCC	CAC	AGT	GGA	TCA	CCC	TTA	GCC	TCC	AAA	AAC	GCC	AAT	GAG	AGA	1574
	Gln	Ser	His	Ser	Gly	Ser	Pro	Leu	Ala	Ser	Lys	Asn	Ala	Asn	Glu	Arg	
	445					450						455					
	AGA	CCC	AGG	GTG	AAA	TCA	AGG	GTG	TCA	GAG	GGC	TCC	ACG	GAT	GAC	AAC	1622
	Arg	Pro	Arg	Val	Lys	Ser	Arg	Val	Ser	Glu	Gly	Ser	Thr	Asp	Asp	Asn	
	460					465						470					

	AGG	TCA	CCC	CAA	TCT	GAC	CCT	TAC	AAC	CAG	CGC	AGG	ATG	TCT	TTC	CTA	1670
	Arg	Ser	Pro	Gln	Ser	Asp	Pro	Tyr	Asn	Gln	Arg	Arg	Met	Ser	Phe	Leu	
	475					480						485					
5	GGC	CTG	TCT	TCA	GGA	AGA	CGC	AGG	GCT	AGC	CAC	GGC	AGT	GTG	TTC	CAC	1718
	Gly	Leu	Ser	Ser	Gly	Arg	Arg	Arg	Arg	Ala	Ser	His	Gly	Ser	Val	Phe	His
	490				495						500					505	
10	TTC	CGA	GCG	CCC	AGC	CAA	GAC	ATC	TCA	TTT	CCT	GAC	GGG	ATC	ACC	CCT	1766
	Phe	Arg	Ala	Pro	Ser	Gln	Asp	Ile	Ser	Phe	Pro	Asp	Gly	Ile	Thr	Pro	
						510				515					520		
15	GAT	GAT	GGG	GTC	TTT	CAC	GGA	GAC	CAG	GAA	AGC	CGT	CGA	GGT	TCC	ATA	1814
	Asp	Asp	Gly	Val	Phe	His	Gly	Asp	Gln	Glu	Ser	Arg	Arg	Gly	Ser	Ile	
						525				530					535		
20	TTG	CTG	GGC	AGG	GGT	GCT	GGG	CAG	ACA	GGT	CCA	CTC	CCC	AGG	AGC	CCA	1862
	Leu	Leu	Gly	Arg	Gly	Ala	Gly	Gln	Thr	Gly	Pro	Leu	Pro	Arg	Ser	Pro	
						540			545			550					
25	CTG	CCT	CAG	TCC	CCC	AAC	CCT	GGC	CGT	AGA	CAT	GGA	GAA	GAG	GGA	CAG	1910
	Leu	Pro	Gln	Ser	Pro	Asn	Pro	Gly	Arg	Arg	His	Gly	Glu	Glu	Gly	Gln	
						555			560			565					
30	CTC	GGA	GTG	CCC	ACT	GGT	GAG	CTT	ACC	GCT	GGA	GCG	CCT	GAA	GGC	CCG	1958
	Leu	Gly	Val	Pro	Thr	Gly	Glu	Leu	Thr	Ala	Gly	Ala	Pro	Glu	Gly	Pro	
						570			575			580				585	
35	GCA	CTC	GAC	ACT	ACA	GGG	CAG	AAG	AGC	TTC	CTG	TCT	GCG	GGC	TAC	TTG	2006
	Ala	Leu	Asp	Thr	Thr	Gly	Gln	Lys	Ser	Phe	Leu	Ser	Ala	Gly	Tyr	Leu	
						590				595					600		
40	AAC	GAA	CCT	TTC	CGA	GCA	CAG	AGG	GCC	ATG	AGC	GTT	GTC	AGT	ATC	ATG	2054
	Asn	Glu	Pro	Phe	Arg	Ala	Gln	Arg	Ala	Met	Ser	Val	Val	Ser	Ile	Met	
						605				610					615		
45	ACT	TCT	GTC	ATT	GAG	GAG	CTT	GAA	GAG	TCT	AAG	CTG	AAG	TGC	CCA	CCC	2102
	Thr	Ser	Val	Ile	Glu	Glu	Leu	Glu	Glu	Ser	Lys	Leu	Lys	Cys	Pro	Pro	
						620			625			630					
50	TGC	TTG	ATC	AGC	TTC	GCT	CAG	AAG	TAT	CTG	ATC	TGG	GAG	TGC	TGC	CCC	2150
	Cys	Leu	Ile	Ser	Phe	Ala	Gln	Lys	Tyr	Leu	Ile	Trp	Gl	Cys	Cys	Pro	
						635			640			645					
55	AAG	TGG	AGG	AAG	TTC	AAG	ATG	GCG	CTG	TTC	GAG	CTG	GTG	ACT	GAC	CCC	2198
	Lys	Trp	Arg	Lys	Phe	Lys	Met	Ala	Leu	Phe	Glu	Leu	Val	Thr	Asp	Pro	
						650			655			660				665	
60	TTC	GCA	GAG	CTT	ACC	ATC	ACC	CTC	TGC	ATC	GTG	GTG	AAC	ACC	GTC	TTC	2246
	Phe	Ala	Glu	Leu	Thr	Ile	Thr	Leu	Cys	Ile	Val	Val	Asn	Thr	Val	Phe	
						670				675					680		
65	ATG	GCC	ATG	GAG	CAC	TAC	CCC	ATG	ACC	GAT	GCC	TTC	GAT	GCC	ATG	CTT	2294
	Met	Ala	Met	Glu	His	Tyr	Pro	Met	Thr	Asp	Ala	Phe	Asp	Ala	Met	Leu	
						685			690						695		
70	CAA	GCC	GGC	AAC	ATT	GTC	TTC	ACC	GTG	TTT	TTC	ACA	ATG	GAG	ATG	GCC	2342
	Gln	Ala	Gly	Asn	Ile	Val	Phe	Thr	Val	Phe	Phe	Thr	Met	Glu	Met	Ala	
						700			705			710					
75	TTC	AAG	ATC	ATT	GCC	TTC	GAC	CCC	TAC	TAT	TAC	TTC	CAG	AAG	AAG	TGG	2390
	Phe	Lys	Ile	Ile	Ala	Phe	Asp	Pro	Tyr	Tyr	Tyr	Phe	Gln	Lys	Lys	Trp	
						715			720			725					

AAT ATC TTC GAC TGT GTC ATC GTC ACC GTG AGC CTT CTG GAG CTG AGT Asn Ile Phe Asp Cys Val Ile Val Thr Val Ser Leu Leu Glu Leu Ser 730 735 740 745	2438
5 GCA TCC AAG AAG GGC AGC CTG TCT GTG CTC CGT TCC TTA CGC TTG GCA Ala Ser Lys Lys Gly Ser Leu Ser Val Leu Arg Ser Leu Arg Leu Ala 750 755 760	2486
10 CTC GAC ACT ACA GGG CAG AAG AGC TTC CTG TCT GCG GGC TAC TTG AAC Leu Asp Thr Thr Gly Gln Lys Ser Phe Leu Ser Ala Gly Tyr Leu Asn 765 770 775	2534
15 GAA CCT TTC CGA GCA CAG AGG GCC ATG AGC GTT GTC AGT ATC ATG ACT Glu Pro Phe Arg Ala Gln Arg Ala Met Ser Val Val Ser Ile Met Thr 780 785 790	2582
20 TCT GTC ATT GAG GAG CTT GAA GAG TCT AAG CTG AAG TGC CCA CCC TGC Ser Val Ile Glu Glu Leu Glu Glu Ser Lys Leu Lys Cys Pro Pro Cys 795 800 805	2630
25 TTG ATC AGC TTC GCT CAG AAG TAT CTG ATC TGG GAG TGC TGC CCC AAG Leu Ile Ser Phe Ala Gln Lys Tyr Leu Ile Trp Glu Cys Cys Pro Lys 810 815 820 825	2678
30 TGG AGG AAG TTC AAG ATG GCG CTG TTC GAG CTG GTG ACT GAC CCC TTC Trp Arg Lys Phe Lys Met Ala Leu Phe Glu Leu Val Thr Asp Pro Phe 830 835 840	2726
35 GCA GAG CTT ACC ATC ACC CTC TGC ATC GTG GTG AAC ACC GTC TTC ATG Ala Glu Leu Thr Ile Thr Leu Cys Ile Val Val Asn Thr Val Phe Met 845 850 855	2774
40 GCC ATG GAG CAC TAC CCC ATG ACC GAT GCC TTC GAT GCC ATG CTT CAA Ala Met Glu His Tyr Pro Met Thr Asp Ala Phe Asp Ala Met Leu Gln 860 865 870	2822
45 GCC GGC AAC ATT GTC TTC ACC GTG TTT TTC ACA ATG GAG ATG GCC TTC Ala Gly Asn Ile Val Phe Thr Val Phe Phe Thr Met Glu Met Ala Phe 875 880 885	2870
50 AAG ATC ATT GCC TTC GAC CCC TAC TAT TAC TTC CAG AAG AAG TGG AAT Lys Ile Ile Ala Phe Asp Pro Tyr Tyr Phe Gln Lys Lys Trp Asn 890 895 900 905	2918
55 ATC TTC GAC TGT GTC ATC GTC ACC GTG AGC CTT CTG GAG CTG AGT GCA Ile Phe Asp Cys Val Ile Val Thr Val Ser Leu Leu Glu Leu Ser Ala 910 915 920	2966
60 TCC AAG AAG GGC AGC CTG TCT GTG CTC CGT TCC TTA CGC TTG CTG CGG Ser Lys Lys Gly Ser Leu Ser Val Leu Arg Ser Leu Arg Leu Leu Arg 925 930 935	3014
GTC TTC AAG CTG GCC AAG TCC TGG CCC ACC CTG AAC ACC CTC ATC AAG Val Phe Lys Leu Ala Lys Ser Trp Pro Thr Leu Asn Thr Leu Ile Lys 940 945 950	3062
ATC ATC GGG AAC TCA GTG GGG GCC CTG GGC AAC CTG ACC TTT ATC CTG Ile Ile Gly Asn Ser Val Gly Ala Leu Gly Asn Leu Thr Phe Ile Leu 955 960 965	3110
65 GCC ATC ATC GTC TTC ATC TTC GCC CTG GTC GGA AAG CAG CTT CTC TCA Ala Ile Ile Val Phe Ile Phe Ala Leu Val Gly Lys Gln Leu Leu Ser 970 975 980 985	3158

	GAG GAC TAC GGG TGC CGC AAG GAC GGC GTC TCC GTG TGG AAC GGC GAG Glu Asp Tyr Gly Cys Arg Lys Asp Gly Val Ser Val Trp Asn Gly Glu 990 995 1000	3206
5	AAG GTC CGC TGG CAC ATG TGT GAC TTC TTC CAT TCC TTC CTG GTC GTC Lys Leu Arg Trp His Met Cys Asp Phe Phe His Ser Phe Leu Val Val 1005 1010 1015	3254
10	TTC CGA ATC CTC TGC GGG GAG TGG ATC GAG AAC ATG TGG GTC TGC ATG Phe Arg Ile Leu Cys Gly Glu Trp Ile Glu Asn Met Trp Val Cys Met 1020 1025 1030	3302
15	GAG GTC AGC GAG AAA TCC ATC TGC CTC ATC CTC TTC TTG ACT GTG ATG Glu Val Ser Gln Lys Ser Ile Cys Leu Ile Leu Phe Leu Thr Val Met 1035 1040 1045	3350
20	GTG CTG GGC AAC GTA GTG GTG CTC AAC CTT TTC ATC GCT TTA CTG CTG Val Leu Gly Asn Leu Val Val Leu Asn Leu Phe Ile Ala Leu Leu Leu 1050 1055 1060 1065	3398
25	AAC TCC TTC AGC GCG GAC AAC CTC ACG GCT CCA GAG GAT GAC GGG GAG Asn Ser Phe Ser Ala Asp Asn Leu Thr Ala Pro Glu Asp Asp Gly Glu 1070 1075 1080	3446
30	GTG AAC AAC TTG CAG TTA GCA CTG GCC AGG ATC CAG GTA CTT GGC CAT Val Asn Asn Leu Gln Leu Ala Leu Ala Arg Ile Gln Val Leu Gly His 1085 1090 1095	3494
35	CGG GCC AGC AGG GCC ATC GCC AGT TAC ATC AGC AGC CAC TGC CGA TTC Arg Ala Ser Arg Ala Ile Ala Ser Tyr Ile Ser Ser His Cys Arg Phe 1100 1105 1110	3542
40	CGC TGG CCC AAG GTG GAG ACC CAG CTG GGC ATG AAG CCC CCA CTC ACC Arg Trp Pro Lys Val Glu Thr Gln Leu Gly Met Lys Pro Pro Leu Thr 1115 1120 1125	3590
45	AGC TCA GAG GCC AAG AAC CAC ATT GCC ACT GAT GCT GTC AGT GCT GCA Ser Ser Glu Ala Lys Asn His Ile Ala Thr Asp Ala Val Ser Ala Ala 1130 1135 1140 1145	3638
50	GTG GGG AAC CTG ACA AAG CCA GCT CTC AGT AGC CCC AAG GAG AAT CAC Val Gly Asn Leu Thr Lys Pro Ala Leu Ser Ser Pro Lys Glu Asn His 1150 1155 1160	3686
55	GGG GAC TTC ATC ACT GAT CCC AAC GTG TGG GTC TCT GTG CCC ATT GCT Gly Asp Phe Ile Thr Asp Pro Asn Val Trp Val Ser Val Pro Ile Ala 1165 1170 1175	3734
60	GAG GGG GAA TCT GAC CTC GAC GAG CTC GAG GAA GAT ATG GAG CAG GCT Glu Gly Glu Ser Asp Leu Asp Glu Leu Glu Glu Asp Met Glu Gln Ala 1180 1185 1190	3782
	TCG CAG AGC TCC TGG CAG GAA GAG GAC CCC AAG GGA CAG CAG GAG CAG Ser Gln Ser Ser Trp Gln Glu Glu Asp Pro Lys Gly Gln Gln Glu Gln 1195 1200 1205	3830
	TTG CCA CAA GTC CAA AAG TGT GAA AAC CAC CAG GGA GCC AGA AGC CCA Leu Pro Gln Val Gln Lys Cys Glu Asn His Gln Ala Ala Arg Ser Pro 1210 1215 1220 1225	3878
	GCC TCC ATG ATG TCC TCT GAG GAC CTG GCT CCA TAC CTG GGT GAG AGC Ala Ser Met Met Ser Ser Glu Asp Leu Ala Pro Tyr Leu Gly Glu Ser 1230 1235 1240	3926

	TGG AAG AGG AAG GAT AGC CCT CAG GTC CCT GCC GAG GGA GTG GAT GAC Trp Lys Arg Lys Asp Ser Pro Gln Val Pro Ala Glu Gly Val Asp Asp 1245 1250 1255	3974
5	ACG AGC TCC TCT GAG GGC AGC ACG GTG GAC TGC CCG GAC CCA GAG GAA Thr Ser Ser Ser Glu Gly Ser Thr Val Asp Cys Pro Asp Pro Glu Glu 1260 1265 1270	4022
10	ATC CTG AGG AAG ATC CCC GAG CTG GCA GAT GAC CTG GAC GAG CCC GAT Ile Leu Arg Lys Ile Pro Glu Leu Ala Asp Asp Leu Asp Glu Pro Asp 1275 1280 1285	4070
15	GAC TGT TTC ACA GAA GGC TGC ACT CGC CGC TGT CCC TGC TGC AAC GTG Asp Cys Phe Thr Glu Gly Cys Thr Arg Arg Cys Pro Cys Cys Asn Val 1290 1295 1300 1305	4118
20	AAT ACT AGC AAG TCT CCT TGG GCC ACA GGC TGG CAG GTG CGC AAG ACC Asn Thr Ser Lys Ser Pro Trp Ala Thr Gly Trp Gln Val Arg Lys Thr 1310 1315 1320	4166
25	TGC TAC CGC ATC GTG GAG CAC AGC TGG TTT GAG AGT TTC ATC ATC TTC Cys Tyr Arg Ile Val Glu His Ser Trp Phe Glu Ser Phe Ile Ile Phe 1325 1330 1335	4214
30	ATG ATC CTG CTC AGC AGT GGA GCG CTG GCC TTT GAG GAT AAC TAC CTG Met Ile Leu Ser Ser Gly Ala Leu Ala Phe Glu Asp Asn Tyr Leu 1340 1345 1350	4262
35	GAA GAG AAA CCC CGA GTG AAG TCC GTG CTG GAG TAC ACT GAC CGA GTG Glu Glu Lys Pro Arg Val Lys Ser Val Leu Glu Tyr Thr Asp Arg Val 1355 1360 1365	4310
40	TTC ACC TTC ATC TTC GTC TTT GAG ATG CTG CTC AAG TGG GTA GCC TAT Phe Thr Phe Ile Phe Val Phe Glu Met Leu Leu Lys Trp Val Ala Tyr 1370 1375 1380 1385	4358
45	GGC TTC AAA AAG TAT TTC ACC AAT GCC TGG TGC TGG CTG GAC TTC CTC Gly Phe Lys Lys Tyr Phe Thr Asn Ala Trp Cys Trp Leu Asp Phe Leu 1390 1395 1400	4406
50	ATT GTG AAC ATC TCC CTG ACA AGC CTC ATA GCG AAG ATC CTT GAG TAT Ile Val Asn Ile Ser Leu Thr Ser Leu Ile Ala Lys Ile Leu Glu Tyr 1405 1410 1415	4454
55	TCC GAC GTG GCG TCC ATC AAA GCC CTT CGG ACT CTC CGT GCC CTC CGA Ser Asp Val Ala Ser Ile Lys Ala Leu Arg Thr Leu Arg Ala Leu Arg 1420 1425 1430	4502
60	CCG CTG CGG GCT CTG TCT CGA TTC GAA GGC ATG AGG GTA GTG GTG GAT Pro Leu Arg Ala Leu Ser Arg Phe Glu Gly Met Arg Val Val Val Asp 1435 1440 1445	4550
	GCC CTC GTG GGC GCC ATC CCC TCC ATC ATG AAC GTC CTC CTC GTC TGC Ala Leu Val Gly Ala Ile Pro Ser Ile Met Asn Val Leu Leu Val Cys 1450 1455 1460 1465	4598
	CTC ATC TTC TGG CTC ATC TTC AGC ATC ATG GGC GTG AAC CTC TTC GCC Leu Ile Phe Trp Leu Ile Phe Ser Ile Met Gly Val Asn Leu Phe Ala 1470 1475 1480	4646
	GGG AAA TTT TCG AAG TGC GTC GAC ACC AGA AAT AAC CCA TTT TCC AAC Gly Lys Phe Ser Lys Cys Val Asp Thr Arg Asn Asn Pro Phe Ser Asn 1485 1490 1495	4694

	GTC AAT TCG ACG ATG GTG AAT AAC AAG TCC GAG TGT CAC AAT CAA AAC Val Asn Ser Thr Met Val Asn Asn Lys Ser Glu Cys His Asn Gln Asn 1500 1505 1510	4742
5	AGC ACC GGC CAC TTC TTC TGG GTC AAC GTC AAA GTC AAC TTC GAC AAC Ser Thr Gly His Phe Phe Trp Val Asn Val Lys Val Asn Phe Asp Asn 1515 1520 1525	4790
10	GTC GCT ATG GGC TAC CTC GCA CTT CTT CAG GTG GCA ACC TTC AAA GGC Val Ala Met Gly Tyr Leu Ala Leu Leu Gln Val Ala Thr Phe Lys Gly 1530 1535 1540 1545	4838
15	TGG ATG GAC ATA ATG TAT GCA GCT GTT GAT TCC GGA GAG ATC AAC AGT Trp Met Asp Ile Met Tyr Ala Ala Val Asp Ser Gly Glu Ile Asn Ser 1550 1555 1560	4886
20	CAG CCT AAC TGG GAG AAC AAC TTG TAC ATG TAC CTG TAC TTC GTC GTT Gln Pro Asn Trp Glu Asn Asn Leu Tyr Met Tyr Leu Tyr Phe Val Val 1565 1570 1575	4934
25	TTC ATC ATT TTC GGT GGC TTG TTC ACG CTG AAT CTC TTT GTT GGG GTC Phe Ile Ile Phe Gly Gly Phe Thr Leu Asn Leu Phe Val Gly Val 1580 1585 1590	4982
30	ATA ATC GAC AAC TTC AAC CAA CAG AAA AAA AAG CTA GGA GGC CAG GAC Ile Ile Asp Asn Phe Asn Gln Gln Lys Lys Lys Leu Gly Gly Gln Asp 1595 1600 1605	5030
35	ATC TTC ATG ACA GAA GAG CAG AAG TAC TAC AAT GCC ATG AAG AAG Ile Phe Met Thr Glu Glu Gln Lys Tyr Tyr Asn Ala Met Lys Lys 1610 1615 1620 1625	5078
40	CTG GGC TCC AAG AAA CCC CAG AAG CCC ATC CCA CGG CCC CTG AAT AAG Leu Gly Ser Lys Lys Pro Gln Lys Pro Ile Pro Arg Pro Leu Asn Lys 1630 1635 1640	5126
45	TAC CAA GGC TTC GTG TTT GAC ATC GTG ACC AGG CAA GCC TTT GAC ATC Tyr Gln Gly Phe Val Phe Asp Ile Val Thr Arg Gln Ala Phe Asp Ile 1645 1650 1655	5174
50	ATC ATC ATG GTT CTC ATC TGC CTC AAC ATG ATC ACC ATG ATG GTG GAG Ile Ile Met Val Leu Ile Cys Leu Asn Met Ile Thr Met Met Val Glu 1660 1665 1670	5222
55	ACC GAC GAG CAG GGC GAG GAG AAG ACG AAG GTT CTG GGC AGA ATC AAC Thr Asp Glu Gln Gly Glu Glu Lys Thr Lys Val Leu Gly Arg Ile Asn 1675 1680 1685	5270
60	CAG TTC TTT GTG GCC GTC TTC ACG GGC GAG TGT GTG ATG AAG ATG TTC Gln Phe Phe Val Ala Val Phe Thr Gly Glu Cys Val Met Lys Met Phe 1690 1695 1700 1705	5318
	GCC CTG CGA CAG TAC TAC TTC ACC AAC GGC TGG AAC GTG TTC GAC TTC Ala Leu Arg Gln Tyr Tyr Phe Thr Asn Gly Trp Asn Val Phe Asp Phe 1710 1715 1720	5366
	ATA GTG GTG ATC CTG TCC ATT GGG AGT CTG CTG TTT TCT GCA ATC CTT Ile Val Val Ile Leu Ser Ile Gly Ser Leu Leu Phe Ser Ala Ile Leu 1725 1730 1735	5414
	AAG TCA CTG GAA AAC TAC TTC TCC CCG ACG CTC TTC CGG GTC ATC CGT Lys Ser Leu Glu Asn Tyr Phe Ser Pro Thr Leu Phe Arg Val Ile Arg 1740 1745 1750	5462

	CTG GCC AGG ATC GGC CGC ATC CTC AGG CTG ATC CGA GCA GCC AAG GGG Leu Ala Arg Ile Gly Arg Ile Leu Arg Leu Ile Arg Ala Ala Lys Gly 1755 1760 1765	5510
5	ATT CGC ACG CTG CTC TTC GCC CTC ATG ATG TCC CTG CCC GCC CTC TTC Ile Arg Thr Leu Leu Phe Ala Leu Met Met Ser Leu Pro Ala Leu Phe 1770 1775 1780 1785	5558
10	AAC ATC GGC CTC CTC TTC CTC GTC ATG TTC ATC TAC TCC ATC TTC Asn Ile Gly Leu Leu Phe Leu Val Met Phe Ile Tyr Ser Ile Phe 1790 1795 1800	5606
15	GGC ATG GCC AGC TTC GCT AAC GTC GTG GAC GAG GCC GGC ATC GAC GAC Gly Met Ala Ser Phe Ala Asn Val Val Asp Glu Ala Gly Ile Asp Asp 1805 1810 1815	5654
20	ATG TTC AAC TTC AAG ACC TTT GGC AAC AGC ATG CTG TGC CTG TTC CAG Met Phe Asn Phe Lys Thr Phe Gly Asn Ser Met Leu Cys Leu Phe Gln 1820 1825 1830	5702
25	ATC ACC ACC TCG GCC GGC TGG GAC GGC CTC CTC AGC CCC ATC CTC AAC Ile Thr Thr Ser Ala Gly Trp Asp Gly Leu Leu Ser Pro Ile Leu Asn 1835 1840 1845	5750
30	ACG GGG CCT CCC TAC TGC GAC CCC AAC CTG CCC AAC AGC AAC GGC TCC Thr Gly Pro Pro Tyr Cys Asp Pro Asn Leu Pro Asn Ser Asn Gly Ser 1850 1855 1860 1865	5798
35	CGG GGG AAC TGC GGG AGC CCG GCG GTG GGC ATC ATC TTC TTC ACC ACC Arg Gly Asn Cys Gly Ser Pro Ala Val Gly Ile Ile Phe Phe Thr Thr 1870 1875 1880	5846
40	TAC ATC ATC ATC TCC TTC CTC ATC GTG GTC AAC ATG TAC ATC GCA GTG Tyr Ile Ile Ile Ser Phe Leu Ile Val Val Asn Met Tyr Ile Ala Val 1885 1890 1895	5894
45	ATT CTG GAG AAC TTC AAC GTA GCC ACC GAG GAG AGC ACG GAG CCC CTG Ile Leu Glu Asn Phe Asn Val Ala Thr Glu Glu Ser Thr Glu Pro Leu 1900 1905 1910	5942
50	AGC GAG GAC GAC TTC GAC ATG TTC TAT GAG ACC TGG GAG AAG TTC GAC Ser Glu Asp Asp Phe Asp Met Phe Tyr Glu Thr Trp Glu Lys Phe Asp 1915 1920 1925	5990
55	CCG GAG GCC ACC CAG TTC ATT GCC TTT TCT GCC CTC TCA GAC TTC GCG Pro Glu Ala Thr Gln Phe Ile Ala Phe Ser Ala Leu Ser Asp Phe Ala 1930 1935 1940 1945	6038
60	GAC ACG CTC TCC GGC CCT CTT AGA ATC CCC AAA CCC AAC CAG AAT ATA Asp Thr Leu Ser Gly Pro Leu Arg Ile Pro Lys Pro Asn Gln Asn Ile 1950 1955 1960	6086
65	TTA ATC CAG ATG GAC CTG CCG TTG GTC CCC GGG GAT AAG ATC GAC TGT Leu Ile Gln Met Asp Leu Pro Leu Val Pro Gly Asp Lys Ile His Cys 1965 1970 1975	6134
70	CTG GAC ATC CTT TTT GCC TTC ACA AAG AAC GTC TTG GGA GAA TCC GGG Leu Asp Ile Leu Phe Ala Phe Thr Lys Asn Val Leu Gly Glu Ser Gly 1980 1985 1990	6182
75	GAG TTG GAC TCC CTG AAG ACC AAT ATG GAA GAG AAG TTT ATG GCG ACC Glu Leu Asp Ser Leu Lys Thr Asn Met Glu Glu Lys Phe Met Ala Thr 1995 2000 2005	6230

AAT CTC TCC AAA GCA TCC TAT GAA CCA ATA GCC ACC ACC CTC CGG TGG Asn Leu Ser Lys Ala Ser Tyr Glu Pro Ile Ala Thr Thr Leu Arg Trp 2010 2015 2020 2025	6278
AAG CAG GAA GAC CTC TCA GCC ACA GTC ATT CAA AAG GCC TAC CGG AGC Lys Gln Glu Asp Leu Ser Ala Thr Val Ile Gln Lys Ala Tyr Arg Ser 2030 2035 2040	6326
TAC ATG CTG CAC CGC TCC TTG ACA CTC TCC AAC ACC CTG CAT GTG CCC Tyr Met Leu His Arg Ser Leu Thr Leu Ser Asn Thr Leu His Val Pro 2045 2050 2055	6374
AGG GCT GAG GAG GAT GGC GTG TCA CTT CCC GGG GAA GGC TAC AGT ACA Arg Ala Glu Glu Asp Gly Val Ser Leu Pro Gly Glu Gly Tyr Ser Thr 2060 2065 2070	6422
TTC ATG GCA AAC AGT GGA CTC CCG GAC AAA TCA GAA ACT GCC TCT GCT Phe Met Ala Ash Ser Gly Leu Pro Asp Lys Ser Glu Thr Ala Ser Ala 2075 2080 2085	6470
ACG TCT TTC CCG CCA TCC TAT GAC AGT GTC ACC AGG GGC CTG AGT GAC Thr Ser Phe Pro Pro Ser Tyr Asp Ser Val Thr Arg Gly Leu Ser Asp 2090 2095 2100 2105	6518
CGG GCC AAC ATT AAC CCA TCT AGC TCA ATG CAA AAT GAA GAT GAG GTC Arg Ala Asn Ile Asn Pro Ser Ser Ser Met Gln Asn Glu Asp Glu Val 2110 2115 2120	6566
GCT GCT AAG GAA GGA AAC AGC CCT GGA CCT CAG TGAAGGCACT CAGGCATGCA Ala Ala Lys Glu Gly Asn Ser Pro Gly Pro Gln 2125 2130	6619
CAGGGCAGGT TCCAATGTCT TTCTCTGCTG TACTAACTCC TTCCCTCTGG AGGTGGCACC	6679
AACCTCCAGC CTCCACCAAT GCATGTCACT GGTCATGGTG TCAGAACTGA ATGGGGACAT	6739
CCTTGAGAAA GCCCCCACCC CAATAGGAAT CAAAAGCCAA GGATACTCCT CCATTCTGAC	6799
GTCCTTCCG AGTTCCCAGA AGATGTCATT GCTCCCTTCT GTTGTGACC AGAGACGTGA	6859
TTCACCAACT TCTCGGAGCC AGAGACACAT AGCAAAGACT TTTCTGCTGG TGTCGGGCAG	6919
TCTTAGAGAA GTCACGTAGG GGTTGGTACT GAGAATTAGG GTTGCATGA CTGCATGCTC	6979
ACAGCTGCCG GACAATACCT GTGAGTCGGC CATTAAAATT AATATTTTA AAGTAAAAAA AAAAAAAAAA AAA	7039 7052
50 (2) INFORMATION FOR SEQ ID NO:6:	
55 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 2132 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear	
60 (ii) MOLECULE TYPE: protein	
65 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:	
Met Glu Leu Pro Phe Ala Ser Val Gly Thr Thr Asn Phe Arg Arg Phe 1 5 10 15	

Thr Pro Glu Ser Leu Ala Glu Ile Glu Lys Gln Ile Ala Ala His Arg
 20 25 30

Ala Ala Lys Lys Ala Arg Thr Lys His Arg Gly Gln Glu Asp Lys Gly
 5 35 40 45

Glu Lys Pro Arg Pro Gln Leu Asp Leu Lys Asp Cys Asn Gln Leu Pro
 50 55 60

10 Lys Phe Tyr Gly Glu Leu Pro Ala Glu Leu Val Gly Glu Pro Leu Glu
 65 70 75 80

Asp Leu Asp Pro Phe Tyr Ser Thr His Arg Thr Phe Met Val Leu Asn
 15 85 90 95

Lys Ser Arg Thr Ile Ser Arg Phe Ser Ala Thr Trp Ala Leu Trp Leu
 100 105 110

20 Phe Ser Pro Phe Asn Leu Ile Arg Arg Thr Ala Ile Lys Val Ser Val
 115 120 125

His Ser Trp Phe Ser Ile Phe Ile Thr Ile Thr Ile Leu Val Asn Cys
 130 135 140

25 Val Cys Met Thr Arg Thr Asp Leu Pro Glu Lys Val Glu Tyr Val Phe
 145 150 155 160

Thr Val Ile Tyr Thr Phe Glu Ala Leu Ile Lys Ile Leu Ala Arg Gly
 30 165 170 175

Phe Cys Leu Asn Glu Phe Thr Tyr Leu Arg Asp Pro Trp Asn Trp Leu
 180 185 190

Asp Phe Ser Val Ile Thr Leu Ala Tyr Val Gly Ala Ala Ile Asp Leu
 35 195 200 205

Arg Gly Ile Ser Gly Leu Arg Thr Phe Arg Val Leu Arg Ala Leu Lys
 210 215 220

40 Thr Val Ser Val Ile Pro Gly Leu Lys Val Ile Val Gly Ala Leu Ile
 225 230 235 240

His Ser Val Arg Lys Leu Ala Asp Val Thr Ile Leu Thr Val Phe Cys
 45 245 250 255

Leu Ser Val Phe Ala Leu Val Gly Leu Gln Leu Phe Lys Gly Asn Leu
 50 260 265 270

Lys Asn Lys Cys Ile Arg Asn Gly Thr Asp Pro His Lys Ala Asp Asn
 275 280 285

Leu Ser Ser Glu Met Ala Glu Tyr Ile Phe Ile Lys Pro Gly Thr Thr
 55 290 295 300

Asp Pro Leu Leu Cys Gly Asn Gly Ser Asp Ala Gly His Cys Pro Gly
 305 310 315 320

Gly Tyr Val Cys Leu Lys Thr Pro Asp Asn Pro Asp Phe Asn Tyr Thr
 60 325 330 335

Ser Phe Asp Ser Phe Ala Trp Ala Phe Leu Ser Leu Phe Arg Leu Met
 340 345 350

Thr Gln Asp Ser Trp Glu Arg Leu Tyr Gln Gln Thr Leu Arg Ala Ser
355 360 365

Gly Lys Met Tyr Met Val Phe Phe Val Leu Val Ile Phe Leu Gly Ser
5 370 375 380

Phe Tyr Leu Val Asn Leu Ile Leu Ala Val Val Thr Met Ala Tyr Glu
385 390 395 400

10 Glu Gln Ser Gln Ala Thr Ile Ala Glu Ile Glu Ala Lys Glu Lys Lys
405 410 415

Phe Gln Glu Ala Leu Glu Val Leu Gln Lys Glu Gln Glu Val Leu Ala
15 420 425 430

Ala Leu Gly Ile Asp Thr Thr Ser Leu Gln Ser His Ser Gly Ser Pro
435 440 445

20 Leu Ala Ser Lys Asn Ala Asn Glu Arg Arg Pro Arg Val Lys Ser Arg
450 455 460

Val Ser Glu Gly Ser Thr Asp Asp Asn Arg Ser Pro Gln Ser Asp Pro
25 465 470 475 480

Tyr Asn Gln Arg Arg Met Ser Phe Leu Gly Leu Ser Ser Gly Arg Arg
485 490 495

Arg Ala Ser His Gly Ser Val Phe His Phe Arg Ala Pro Ser Gln Asp
30 500 505 510

Ile Ser Phe Pro Asp Gly Ile Thr Pro Asp Asp Gly Val Phe His Gly
515 520 525

Asp Gln Glu Ser Arg Arg Gly Ser Ile Leu Leu Gly Arg Gly Ala Gly
35 530 535 540

Gln Thr Gly Pro Leu Pro Arg Ser Pro Leu Pro Gln Ser Pro Asn Pro
545 550 555 560

40 Gly Arg Arg His Gly Glu Glu Gly Gln Leu Gly Val Pro Thr Gly Glu
565 570 575

Leu Thr Ala Gly Ala Pro Glu Gly Pro Ala Leu Asp Thr Thr Gly Gln
45 580 585 590

Lys Ser Phe Leu Ser Ala Gly Tyr Leu Asn Glu Pro Phe Arg Ala Gln
595 600 605

Arg Ala Met Ser Val Val Ser Ile Met Thr Ser Val Ile Glu Glu Leu
50 610 615 620

Glu Glu Ser Lys Leu Lys Cys Pro Pro Cys Leu Ile Ser Phe Ala Gln
625 630 635 640

55 Lys Tyr Leu Ile Trp Glu Cys Cys Pro Lys Trp Arg Lys Phe Lys Met
645 650 655

Ala Leu Phe Glu Leu Val Thr Asp Pro Phe Ala Glu Leu Thr Ile Thr
660 665 670

60 Leu Cys Ile Val Val Asn Thr Val Phe Met Ala Met Glu His Tyr Pro
675 680 685

Met Thr Asp Ala Phe Asp Ala Met Leu Gln Ala Gly Asn Ile Val Phe
 690 695 700

5 Thr Val Phe Phe Thr Met Glu Met Ala Phe Lys Ile Ile Ala Phe Asp
 705 710 715 720

Pro Tyr Tyr Tyr Phe Gln Lys Lys Trp Asn Ile Phe Asp Cys Val Ile
 725 730 735

10 Val Thr Val Ser Leu Leu Glu Leu Ser Ala Ser Lys Lys Gly Ser Leu
 740 745 750

Ser Val Leu Arg Ser Leu Arg Leu Ala Leu Asp Thr Thr Gly Gln Lys
 755 760 765

15 Ser Phe Leu Ser Ala Gly Tyr Leu Asn Glu Pro Phe Arg Ala Gln Arg
 770 775 780

20 Ala Met Ser Val Val Ser Ile Met Thr Ser Val Ile Glu Glu Leu Glu
 785 790 795 800

Glu Ser Lys Leu Lys Cys Pro Pro Cys Leu Ile Ser Phe Ala Gln Lys
 805 810 815

25 Tyr Leu Ile Trp Glu Cys Cys Pro Lys Trp Arg Lys Phe Lys Met Ala
 820 825 830

Leu Phe Glu Leu Val Thr Asp Pro Phe Ala Glu Leu Thr Ile Thr Leu
 835 840 845

30 Cys Ile Val Val Asn Thr Val Phe Met Ala Met Glu His Tyr Pro Met
 850 855 860

Thr Asp Ala Phe Asp Ala Met Leu Gln Ala Gly Asn Ile Val Phe Thr
 865 870 875 880

Val Phe Phe Thr Met Glu Met Ala Phe Lys Ile Ile Ala Phe Asp Pro
 885 890 895

40 Tyr Tyr Tyr Phe Gln Lys Lys Trp Asn Ile Phe Asp Cys Val Ile Val
 900 905 910

Thr Val Ser Leu Leu Glu Leu Ser Ala Ser Lys Lys Gly Ser Leu Ser
 915 920 925

45 Val Leu Arg Ser Leu Arg Leu Leu Arg Val Phe Lys Leu Ala Lys Ser
 930 935 940

50 Trp Pro Thr Leu Asn Thr Leu Ile Lys Ile Ile Gly Asn Ser Val Gly
 945 950 955 960

Ala Leu Gly Asn Leu Thr Phe Ile Leu Ala Ile Ile Val Phe Ile Phe
 965 970 975

55 Ala Leu Val Gly Lys Gln Leu Leu Ser Glu Asp Tyr Gly Cys Arg Lys
 980 985 990

60 Asp Gly Val Ser Val Trp Asn Gly Glu Lys Leu Arg Trp His Met Cys
 995 1000 1005

Asp Phe Phe His Ser Phe Leu Val Val Phe Arg Ile Leu Cys Gly Glu
 1010 1015 1020

T_rp Ile Glu Asn Met Trp Val Cys Met Glu Val Ser Gln Lys Ser Ile
 1025 1030 1035 1040

5 Cys Leu Ile Leu Phe Leu Thr Val Met Val Leu Gly Asn Leu Val Val
 1045 1050 1055

Leu Asn Leu Phe Ile Ala Leu Leu Asn Ser Phe Ser Ala Asp Asn
 1060 1065 1070

10 Leu Thr Ala Pro Glu Asp Asp Gly Glu Val Asn Asn Leu Gln Leu Ala
 1075 1080 1085

Leu Ala Arg Ile Gln Val Leu Gly His Arg Ala Ser Arg Ala Ile Ala
 1090 1095 1100

15 Ser Tyr Ile Ser Ser His Cys Arg Phe Arg Trp Pro Lys Val Glu Thr
 1105 1110 1115 1120

20 Gln Leu Gly Met Lys Pro Pro Leu Thr Ser Ser Glu Ala Lys Asn His
 1125 1130 1135

Ile Ala Thr Asp Ala Val Ser Ala Ala Val Gly Asn Leu Thr Lys Pro
 1140 1145 1150

25 Ala Leu Ser Ser Pro Lys Glu Asn His Gly Asp Phe Ile Thr Asp Pro
 1155 1160 1165

Asn Val Trp Val Ser Val Pro Ile Ala Glu Gly Glu Ser Asp Leu Asp
 1170 1175 1180

30 Glu Leu Glu Glu Asp Met Glu Gln Ala Ser Gln Ser Ser Trp Gln Glu
 1185 1190 1195 1200

Glu Asp Pro Lys Gly Gln Gln Glu Leu Pro Gln Val Gln Lys Cys
 1205 1210 1215

Glu Asn His Gln Ala Ala Arg Ser Pro Ala Ser Met Met Ser Ser Glu
 1220 1225 1230

40 Asp Leu Ala Pro Tyr Leu Gly Glu Ser Trp Lys Arg Lys Asp Ser Pro
 1235 1240 1245

Gln Val Pro Ala Glu Gly Val Asp Asp Thr Ser Ser Ser Glu Gly Ser
 1250 1255 1260

45 Thr Val Asp Cys Pro Asp Pro Glu Glu Ile Leu Arg Lys Ile Pro Glu
 1265 1270 1275 1280

Leu Ala Asp Asp Leu Asp Glu Pro Asp Asp Cys Phe Thr Glu Gly Cys
 1285 1290 1295

50 Thr Arg Arg Cys Pro Cys Cys Asn Val Asn Thr Ser Lys Ser Pro Trp
 1300 1305 1310

Ala Thr Gly Trp Gln Val Arg Lys Thr Cys Tyr Arg Ile Val Glu His
 1315 1320 1325

Ser Trp Phe Glu Ser Phe Ile Ile Phe Met Ile Leu Leu Ser Ser Gly
 1330 1335 1340

60 Ala Leu Ala Phe Glu Asp Asn Tyr Leu Glu Glu Lys Pro Arg Val Lys
 1345 1350 1355 1360

Ser Val Leu Glu Tyr Thr Asp Arg Val Phe Thr Phe Ile Phe Val Phe
 1365 1370 1375

Glu Met Leu Leu Lys Trp Val Ala Tyr Gly Phe Lys Lys Tyr Phe Thr
 1380 1385 1390

5 Asn Ala Trp Cys Trp Leu Asp Phe Leu Ile Val Asn Ile Ser Leu Thr
 1395 1400 1405

Ser Leu Ile Ala Lys Ile Leu Glu Tyr Ser Asp Val Ala Ser Ile Lys
 1410 1415 1420

10 Ala Leu Arg Thr Leu Arg Ala Leu Arg Pro Leu Arg Ala Leu Ser Arg
 1425 1430 1435 1440

15 Phe Glu Gly Met Arg Val Val Val Asp Ala Leu Val Gly Ala Ile Pro
 1445 1450 1455

Ser Ile Met Asn Val Leu Leu Val Cys Leu Ile Phe Trp Leu Ile Phe
 1460 1465 1470

20 Ser Ile Met Gly Val Asn Leu Phe Ala Gly Lys Phe Ser Lys Cys Val
 1475 1480 1485

Asp Thr Arg Asn Asn Pro Phe Ser Asn Val Asn Ser Thr Met Val Asn
 1490 1495 1500

25 Asn Lys Ser Glu Cys His Asn Gln Asn Ser Thr Gly His Phe Phe Trp
 1505 1510 1515 1520

30 Val Asn Val Lys Val Asn Phe Asp Asn Val Ala Met Gly Tyr Leu Ala
 1525 1530 1535

Leu Leu Gln Val Ala Thr Phe Lys Gly Trp Met Asp Ile Met Tyr Ala
 1540 1545 1550

35 Ala Val Asp Ser Gly Glu Ile Asn Ser Gln Pro Asn Trp Glu Asn Asn
 1555 1560 1565

Leu Tyr Met Tyr Leu Tyr Phe Val Val Phe Ile Ile Phe Gly Gly Phe
 1570 1575 1580

40 Phe Thr Leu Asn Leu Phe Val Gly Val Ile Ile Asp Asn Phe Asn Gln
 1585 1590 1595 1600

45 Gln Lys Lys Lys Leu Gly Gly Gln Asp Ile Phe Met Thr Glu Glu Gln
 1605 1610 1615

Lys Lys Tyr Tyr Asn Ala Met Lys Lys Leu Gly Ser Lys Lys Pro Gln
 1620 1625 1630

50 Lys Pro Ile Pro Arg Pro Leu Asn Lys Tyr Gln Gly Phe Val Phe Asp
 1635 1640 1645

Ile Val Thr Arg Gln Ala Phe Asp Ile Ile Ile Met Val Leu Ile Cys
 1650 1655 1660

55 Leu Asn Met Ile Thr Met Met Val Glu Thr Asp Glu Gln Gly Glu Glu
 1665 1670 1675 1680

Lys Thr Lys Val Leu Gly Arg Ile Asn Gln Phe Phe Val Ala Val Phe
 1685 1690 1695

Thr Gly Glu Cys Val Met Lys Met Phe Ala Leu Arg Gln Tyr Tyr Phe
 1700 1705 1710

Thr Asn Gly Trp Asn Val Phe Asp Phe Ile Val Val Ile Leu Ser Ile
 1715 1720 1725

5 Gly Ser Leu Leu Phe Ser Ala Ile Leu Lys Ser Leu Glu Asn Tyr Phe
 1730 1735 1740

Ser Pro Thr Leu Phe Arg Val Ile Arg Leu Ala Arg Ile Gly Arg Ile
 1745 1750 1755 1760

10 Leu Arg Leu Ile Arg Ala Ala Lys Gly Ile Arg Thr Leu Leu Phe Ala
 1765 1770 1775

Leu Met Met Ser Leu Pro Ala Leu Phe Asn Ile Gly Leu Leu Phe
 1780 1785 1790

15 Leu Val Met Phe Ile Tyr Ser Ile Phe Gly Met Ala Ser Phe Ala Asn
 1795 1800 1805

20 Val Val Asp Glu Ala Gly Ile Asp Asp Met Phe Asn Phe Lys Thr Phe
 1810 1815 1820

Gly Asn Ser Met Leu Cys Leu Phe Gln Ile Thr Thr Ser Ala Gly Trp
 1825 1830 1835 1840

25 Asp Gly Leu Leu Ser Pro Ile Leu Asn Thr Gly Pro Pro Tyr Cys Asp
 1845 1850 1855

30 Pro Asn Leu Pro Asn Ser Asn Gly Ser Arg Gly Asn Cys Gly Ser Pro
 1860 1865 1870

Ala Val Gly Ile Ile Phe Phe Thr Thr Tyr Ile Ile Ile Ser Phe Leu
 1875 1880 1885

35 Ile Val Val Asn Met Tyr Ile Ala Val Ile Leu Glu Asn Phe Asn Val
 1890 1895 1900

Ala Thr Glu Glu Ser Thr Glu Pro Leu Ser Glu Asp Asp Phe Asp Met
 1905 1910 1915 1920

40 Phe Tyr Glu Thr Trp Glu Lys Phe Asp Pro Glu Ala Thr Gln Phe Ile
 1925 1930 1935

45 Ala Phe Ser Ala Leu Ser Asp Phe Ala Asp Thr Leu Ser Gly Pro Leu
 1940 1945 1950

Arg Ile Pro Lys Pro Asn Gln Asn Ile Leu Ile Gln Met Asp Leu Pro
 1955 1960 1965

50 Leu Val Pro Gly Asp Lys Ile His Cys Leu Asp Ile Leu Phe Ala Phe
 1970 1975 1980

Thr Lys Asn Val Leu Gly Glu Ser Gly Glu Leu Asp Ser Leu Lys Thr
 1985 1990 1995 2000

55 Asn Met Glu Glu Lys Phe Met Ala Thr Asn Leu Ser Lys Ala Ser Tyr
 2005 2010 2015

60 Glu Pro Ile Ala Thr Thr Leu Arg Trp Lys Gln Glu Asp Leu Ser Ala
 2020 2025 2030

Thr Val Ile Gln Lys Ala Tyr Arg Ser Tyr Met Leu His Arg Ser Leu
 2035 2040 2045

Thr Leu Ser Asn Thr Leu His Val Pro Arg Ala Glu Glu Asp Gly Val
 2050 2055 2060
 Ser Leu Pro Gly Glu Gly Tyr Ser Thr Phe Met Ala Asn Ser Gly Leu
 5 2065 2070 2075 2080
 Pro Asp Lys Ser Glu Thr Ala Ser Ala Thr Ser Phe Pro Pro Ser Tyr
 2085 2090 2095
 10 Asp Ser Val Thr Arg Gly Leu Ser Asp Arg Ala Asn Ile Asn Pro Ser
 2100 2105 2110
 Ser Ser Met Gln Asn Glu Asp Glu Val Ala Ala Lys Glu Gly Asn Ser
 2115 2120 2125
 15 Pro Gly Pro Gln
 2130

20 (2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6527 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 204..6077

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

TAGCTTGCTT CTGCTAATGC TACCCCAGGC CTTTAGACAG AGAACAGATG GCAGATGGAG	60
40 TTTCTTATTG CCATGCGCAA ACGCTGAGCC CACCTCATGA TCCCGGACCC CATGGTTTC	120
AGTAGACAAC CTGGGCTAACG AAGAGATCTC CGACCTTATA GAGCAGCAAA GAGTGTAAAT	180
45 TCTTCCCCAA GAAGAATGAG AAG ATG GAG CTC CCC TTT GCG TCC GTG GGA	230
Met Glu Leu Pro Phe Ala Ser Val Gly	
1	
5 T	
ACT ACC AAT TTC AGA CGG TTC ACT CCA GAG TCA CTG GCA GAG ATC GAG	278
Thr Thr Asn Phe Arg Arg Phe Thr Pro Glu Ser Leu Ala Glu Ile Glu	
10 15 20 25	
50 AAG CAG ATT GCT CAC CGG GCA GCC AAG AAG GCC AGA ACC AAG CAC	326
Lys Gln Ile Ala Ala His Arg Ala Ala Lys Lys Ala Arg Thr Lys His	
30 35 40	
55 AGA GGA CAG GAG GAC AAG GGC GAG AAG CCC AGG CCT CAG CTG GAC TTG	374
Arg Gly Gln Glu Asp Lys Gly Glu Lys Pro Arg Pro Gln Leu Asp Leu	
45 50 55	
60 AAA GAC TGT AAC CAG CTG CCC AAG TTC TAT GGT GAG CTC CCA GCA GAA	422
Lys Asp Cys Asn Gln Leu Pro Lys Phe Tyr Gly Glu Leu Pro Ala Glu	
60 65 70	

	CTG GTC GGG GAG CCC CTG GAG GAC CTA GAC CCT TTC TAC AGC ACA CAC	470
	Leu Val Gly Glu Pro Leu Glu Asp Leu Asp Pro Phe Tyr Ser Thr His	
75	75 80 85	
5	CGG ACA TTC ATG GTG TTG AAT AAA AGC AGG ACC ATT TCC AGA TTC AGT	518
	Arg Thr Phe Met Val Leu Asn Lys Ser Arg Thr Ile Ser Arg Phe Ser	
90	90 95 100 105	
10	GCC ACT TGG GCC CTG TGG CTC TTC AGT CCC TTC AAC CTG ATC AGA AGA	566
	Ala Thr Trp Ala Leu Trp Leu Phe Ser Pro Phe Asn Leu Ile Arg Arg	
	110 115 120	
15	ACA GCC ATC AAA GTG TCT GTC CAT TCC TGG TTC TCC ATA TTC ATC ACC	614
	Thr Ala Ile Lys Val Ser Val His Ser Trp Phe Ser Ile Phe Ile Thr	
	125 130 135	
20	ATC ACT ATT TTG GTC AAC TGC GTG TGC ATG ACC CGA ACT GAT CTT CCA	662
	Ile Thr Ile Leu Val Asn Cys Val Cys Met Thr Arg Thr Asp Leu Pro	
	140 145 150	
25	GAG AAA GTC GAG TAC GTC TTC ACT GTC ATT TAC ACC TTC GAG GCT CTG	710
	Glu Lys Val Glu Tyr Val Phe Thr Val Ile Tyr Thr Phe Glu Ala Leu	
	155 160 165	
30	CGA GAT CCG TGG AAC TGG CTG GAC TTC AGT GTC ATT ACC TTG GCG TAT	806
	Arg Asp Pro Trp Asn Trp Leu Asp Phe Ser Val Ile Thr Leu Ala Tyr	
	190 195 200	
35	GTG GGT GCA GCG ATA GAC CTC CGA GGA ATC TCA GGC CTG CGG ACA TTC	854
	Val Gly Ala Ala Ile Asp Leu Arg Gly Ile Ser Gly Leu Arg Thr Phe	
	205 210 215	
40	CGA GTT CTC AGA GCC CTG AAA ACT GTT TCT GTG ATC CCA GGA CTG AAG	902
	Arg Val Leu Arg Ala Leu Lys Thr Val Ser Val Ile Pro Gly Leu Lys	
	220 225 230	
45	GTC ATC GTG GGA GCC CTG ATC CAC TCA GTG AGG AAG CTG GCC GAC GTG	950
	Val Ile Val Gly Ala Leu Ile His Ser Val Arg Lys Leu Ala Asp Val	
	235 240 245	
50	ACT ATC CTC ACA GTC TTC TGC CTG AGC GTC TTC GGC TTC GTG GGC CTG	998
	Thr Ile Leu Thr Val Phe Cys Leu Ser Val Phe Ala Leu Val Gly Leu	
	250 255 260 265	
55	CAG CTC TTT AAG GGG AAC CTT AAG AAC AAA TGC ATC AGG AAC GGA ACA	1046
	Gln Leu Phe Lys Gly Asn Leu Lys Asn Lys Cys Ile Arg Asn Gly Thr	
	270 275 280	
60	GAT CCC CAC AAG GCT GAC AAC CTC TCA TCT GAA ATG GCA GAA TAC ATC	1094
	Asp Pro His Lys Ala Asp Asn Leu Ser Ser Glu Met Ala Glu Tyr Ile	
	285 290 295	
	TTC ATC AAG CCT GGT ACT ACG GAT CCC TTA CTG TGC GGC AAT GGG TCT	1142
	Phe Ile Lys Pro Gly Thr Thr Asp Pro Leu Leu Cys Gly Asn Gly Ser	
	300 305 310	
	GAT GCT GGT CAC TGC CCT GGA GGC TAT GTC TGC CTG AAA ACT CCT GAC	1190
	Asp Ala Gly His Cys Pro Gly Gly Tyr Val Cys Leu Lys Thr Pro Asp	
	315 320 325	

AAC CCG GAT TTT AAC TAC ACC AGC TTT GAT TCC TTT GCG TGG GCA TTC	1238
Asn Pro Asp Phe Asn Tyr Thr Ser Phe Asp Ser Phe Ala Trp Ala Phe	
330 335 340 345	
5 CTC TCA CTG TTC CGC CTC ATG ACG CAG GAC TCC TGG GAG CGC CTG TAC	1286
Leu Ser Ile Phe Arg Leu Met Thr Gln Asp Ser Trp Glu Arg Leu Tyr	
350 355 360	
10 CAG CAG ACA CTC CGG GCT TCT GGG AAA ATG TAC ATG GTC TTT TTC GTG	1334
Gln Gln Thr Leu Arg Ala Ser Gly Lys Met Tyr Met Val Phe Phe Val	
365 370 375	
15 CTG GTT ATT TTC CTT GGA TCG TTC TAC CTG GTC AAT TTG ATC TTG GCC	1382
Leu Val Ile Phe Leu Gly Ser Phe Tyr Leu Val Asn Leu Ile Leu Ala	
380 385 390	
20 GTG GTC ACC ATG GCG TAT GAA GAG CAG AGC CAG GCA ACA ATT GCA GAA	1430
Val Val Thr Met Ala Tyr Glu Glu Gln Ser Gln Ala Thr Ile Ala Glu	
395 400 405	
25 ATC GAA GCC AAG GAA AAA AAG TTC CAG GAA GCC CTT GAG GTG CTG CAG	1478
Ile Glu Ala Lys Glu Lys Phe Gln Glu Ala Leu Glu Val Leu Gln	
410 415 420 425	
30 CAG TCC CAC AGT GGA TCA CCC TTA GCC TCC AAA AAC GCC AAT GAG AGA	1526
Gln Ser His Ser Gly Ser Pro Leu Ala Ser Lys Asn Ala Asn Glu Arg	
445 450 455	
35 AGA CCC AGG GTG AAA TCA AGG GTG TCA GAG GGC TCC ACG GAT GAC AAC	1574
Arg Pro Arg Val Lys Ser Arg Val Ser Glu Gly Ser Thr Asp Asp Asn	
460 465 470	
40 AGG TCA CCC CAA TCT GAC CCT TAC AAC CAG CGC AGG ATG TCT TTC CTA	1622
Arg Ser Pro Gln Ser Asp Pro Tyr Asn Gln Arg Arg Met Ser Phe Leu	
475 480 485	
45 GGC CTG TCT TCA GGA AGA CGC AGG GCT AGC CAC GGC AGT GTG TTC CAC	1670
Gly Leu Ser Ser Gly Arg Arg Ala Ser His Gly Ser Val Phe His	
490 495 500 505	
50 GAT GAT GGG GTC TTT CAC GGA GAC CAG GAA AGC CGT CGA GGT TCC ATA	1718
Asp Asp Gly Val Phe His Gly Asp Gln Glu Ser Arg Arg Gly Ser Ile	
525 530 535	
55 TTG CTG GGC AGG GGT GCT GGG CAG ACA GGT CCA CTC CCC AGG AGC CCA	1814
Leu Leu Gly Arg Gly Ala Gly Gln Thr Gly Pro Leu Pro Arg Ser Pro	
540 545 550	
60 CTG CCT CAG TCC CCC AAC CCT GGC CGT AGA CAT GGA GAA GAG GGA CAG	1910
Leu Pro Gln Ser Pro Asn Pro Gly Arg Arg His Gly Glu Glu Gly Gln	
555 560 565	
CTC GGA GTG CCC ACT GGT GAG CTT ACC GCT GGA GCG CCT GAA GGC CCG	1958
Leu Gly Val Pro Thr Gly Glu Leu Thr Ala Gly Ala Pro Glu Gly Pro	
570 575 580 585	

	GCA CTC GAC ACT ACA GGG CAG AAG AGC TTC CTG TCT GCG GGC TAC TTG Ala Leu Asp Thr Thr Gly Gln Lys Ser Phe Leu Ser Ala Gly Tyr Leu 590 595 600	2006
5	AAC GAA CCT TTC CGA GCA CAG AGG GCC ATG AGC GTT GTC AGT ATC ATG Asn Glu Pro Phe Arg Ala Gln Arg Ala Met Ser Val Val Ser Ile Met 605 610 615	2054
10	ACT TCT GTC ATT GAG GAG CTT GAA GAG TCT AAG CTG AAG TGC CCA CCC Thr Ser Val Ile Glu Glu Leu Glu Ser Lys Leu Lys Cys Pro Pro 620 625 630	2102
15	TGC TTG ATC AGC TTC GCT CAG AAG TAT CTG ATC TGG GAG TGC TGC CCC Cys Leu Ile Ser Phe Ala Gln Lys Tyr Leu Ile Trp Glu Cys Cys Pro 635 640 645	2150
20	AAG TGG AGG AAG TTC AAG ATG GCG CTG TTC GAG CTG GTG ACT GAC CCC Lys Trp Arg Lys Phe Lys Met Ala Leu Phe Glu Leu Val Thr Asp Pro 650 655 660 665	2198
25	TTC GCA GAG CTT ACC ATC ACC CTC TGC ATC GTG GTG AAC ACC GTC TTC Phe Ala Glu Leu Thr Ile Thr Leu Cys Ile Val Val Asn Thr Val Phe 670 675 680	2246
30	ATG GCC ATG GAG CAC TAC CCC ATG ACC GAT GCC TTC GAT GCC ATG CTT Met Ala Met Glu His Tyr Pro Met Thr Asp Ala Phe Asp Ala Met Leu 685 690 695	2294
35	CAA GCC GGC AAC ATT GTC TTC ACC GTG TTT TTC ACA ATG GAG ATG GCC Gln Ala Gly Asn Ile Val Phe Thr Val Phe Thr Met Glu Met Ala 700 705 710	2342
40	TTC AAG ATC ATT GCC TTC GAC CCC TAC TAT TAC TTC CAG AAG AAG TGG Phe Lys Ile Ile Ala Phe Asp Pro Tyr Tyr Tyr Phe Gln Lys Lys Trp 715 720 725	2390
45	AAT ATC TTC GAC TGT GTC ATC GTC ACC GTG AGC CTT CTG GAG CTG AGT Asn Ile Phe Asp Cys Val Ile Val Thr Val Ser Leu Leu Glu Leu Ser 730 735 740 745	2438
50	GCA TCC AAG AAG GGC AGC CTG TCT GTG CTC CGT TCC TTA CGC TTG CTG Ala Ser Lys Lys Gly Ser Leu Ser Val Leu Arg Ser Leu Arg Leu Leu 750 755 760	2486
55	CGG GTC TTC AAG CTG GCC AAG TCC TGG CCC ACC CTG AAC ACC CTC ATC Arg Val Phe Lys Leu Ala Lys Ser Trp Pro Thr Leu Asn Thr Leu Ile 765 770 775	2534
60	CAG AAT ATC GGG AAC TCA GTG GGG GCC CTG GGC AAC CTG ACC TTT ATC Lys Ile Ile Gly Asn Ser Val Gly Ala Leu Gly Asn Leu Thr Phe Ile 780 785 790	2582
	CTG GCC ATC ATC GTC TTC ATC TTC GCC CTG GTC GGA AAG CAG CTT CTC Leu Ala Ile Ile Val Phe Ile Phe Ala Leu Val Gly Lys Gln Leu Leu 795 800 805	2630
	TCA GAG GAC TAC GGG TGC CGC AAG GAC GGC GTC TCC GTG TGG AAC GGC Ser Glu Asp Tyr Gly Cys Arg Lys Asp Gly Val Ser Val Trp Asn Gly 810 815 820 825	2678
	GAG AAG CTC CGC TGG CAC ATG TGT GAC TTC TTC CAT TCC TTC CTG GTC Glu Lys Leu Arg Trp His Met Cys Asp Phe Phe His Ser Phe Leu Val 830 835 840	2726

	GTC TTC CGA ATC CTC TGC GGG GAG TGG ATC GAG AAC ATG TGG GTC TGC Val Phe Arg Ile Leu Cys Gly Glu Trp Ile Glu Asn Met Trp Val Cys 845 850 855	2774
5	ATG GAG GTC ACC CAG AAA TCC ATC TGC CTC ATC CTC TTC TTG ACT GTG Met Glu Val Ser Gln Lys Ser Ile Cys Leu Ile Leu Phe Leu Thr Val 860 865 870	2822
10	ATG GTG CTG GGC AAC CTA GTG GTG CTC AAC CTT TTC ATC GCT TTA CTG Met Val Leu Gly Asn Leu Val Val Leu Asn Leu Phe Ile Ala Leu Leu 875 880 885	2870
15	CTG AAC TCC TTC AGC GCG GAC AAC CTC ACG GCT CCA GAG GAT GAC GGG Leu Asn Ser Phe Ser Ala Asp Asn Leu Thr Ala Pro Glu Asp Asp Gly 890 895 900 905	2918
20	GAG GTG AAC AAC TTG CAG TTA GCA CTG GCC AGG ATC CAG GTA CTT GGC Glu Val Asn Asn Leu Gln Leu Ala Leu Ala Arg Ile Gln Val Leu Gly 910 915 920	2966
25	CAT CGG GCC AGC AGG GCC ATC GCC AGT TAC ATC AGC AGC CAC TGC CGA His Arg Ala Ser Arg Ala Ile Ala Ser Tyr Ile Ser Ser His Cys Arg 925 930 935	3014
30	TTC CGC TGG CCC AAG GTG GAG ACC CAG CTG GGC ATG AAG CCC CCA CTC Phe Arg Trp Pro Lys Val Glu Thr Gln Leu Gly Met Lys Pro Pro Leu 940 945 950	3062
35	ACC AGC TCA GAG GCC AAG AAC CAC ATT GCC ACT GAT GCT GTC AGT GCT Thr Ser Ser Glu Ala Lys Asn His Ile Ala Thr Asp Ala Val Ser Ala 955 960 965	3110
40	GCA GTG GGG AAC CTG ACA AAG CCA GCT CTC AGT AGC CCC AAG GAG AAT Ala Val Gly Asn Leu Thr Lys Pro Ala Leu Ser Ser Pro Lys Glu Asn 970 975 980 985	3158
45	CAC GGG GAC TTC ATC ACT GAT CCC AAC GTG TGG GTC TCT GTG CCC ATT His Gly Asp Phe Ile Thr Asp Pro Asn Val Trp Val Ser Val Pro Ile 990 995 1000	3206
50	GCT GAG GGG GAA TCT GAC CTC GAC GAG CTC GAG GAA GAT ATG GAG CAG Ala Glu Gly Glu Ser Asp Leu Asp Glu Leu Glu Glu Asp Met Glu Gln 1005 1010 1015	3254
55	GCT TCG CAG AGC TCC TGG CAG GAA GAG GAC CCC AAG GGA CAG CAG GAC Ala Ser Gln Ser Ser Trp Gln Glu Glu Asp Pro Lys Gly Gln Gln Glu 1020 1025 1030	3302
60	CAG TTG CCA CAA GTC CAA AAG TGT GAA AAC CAC CAG GCA GCC AGA AGC Gln Leu Pro Gln Val Gln Lys Cys Glu Asn His Gln Ala Ala Arg Ser 1035 1040 1045	3350
	CCA GCC TCC ATG ATG TCC TCT GAG GAC CTG GCT CCA TAC CTG GGT GAG Pro Ala Ser Met Met Ser Ser Glu Asp Leu Ala Pro Tyr Leu Gly Glu 1050 1055 1060 1065	3398
	AGC TGG AAG AGG AAG GAT AGC CCT CAG GTC CCT GCC GAG GGA GTG GAT Ser Trp Lys Arg Lys Asp Ser Pro Gln Val Pro Ala Glu Gly Val Asp 1070 1075 1080	3446
	GAC ACG AGC TCC TCT GAG GGC AGC ACG GTG GAC TGC CCG GAC CCA GAG Asp Thr Ser Ser Ser Glu Gly Ser Thr Val Asp Cys Pro Asp Pro Glu 1085 1090 1095	3494

GAA ATC CTG AGG AAG ATC CCC GAG CTG GCA GAT GAC CTG GAC GAG CCC Glu Ile Leu Arg Lys Ile Pro Glu Leu Ala Asp Asp Leu Asp Glu Pro 1100 1105 1110	3542
5 GAT GAC TGT TTC ACA GAA GGC TGC ACT CGC CGC TGT CCC TGC TGC AAC Asp Asp Cys Phe Thr Glu Gly Cys Thr Arg Arg Cys Pro Cys Cys Asn 1115 1120 1125	3590
10 GTG AAT ACT AGC AAG TCT CCT TGG GCC ACA GGC TGG CAG GTG CGC AAG Val Asn Thr Ser Lys Ser Pro Trp Ala Thr Gly Trp Gln Val Arg Lys 1130 1135 1140 1145	3638
15 ACC TGC TAC CGC ATC GTG GAG CAC AGC TGG TTT GAG AGT TTC ATC ATC Thr Cys Tyr Arg Ile Val Glu His Ser Trp Phe Glu Ser Phe Ile Ile 1150 1155 1160	3686
20 TTC ATG ATC CTG CTC AGC AGT GGA GCG CTG GCC TTT GAG GAT AAC TAC Phe Met Ile Leu Ser Ser Gly Ala Leu Ala Phe Glu Asp Asn Tyr 1165 1170 1175	3734
25 CTG GAA GAG AAA CCC CGA GTG AAG TCC GTG CTG GAG TAC ACT GAC CGA Leu Glu Lys Pro Arg Val Lys Ser Val Leu Glu Tyr Thr Asp Arg 1180 1185 1190	3782
30 TAT GGC TTC AAA AAG TAT TTC ACC AAT GCC TGG TGC TGG CTG GAC TTC Tyr Gly Phe Lys Lys Tyr Phe Thr Asn Ala Trp Cys Trp Leu Asp Phe 1210 1215 1220 1225	3878
35 CTC ATT GTG AAC ATC TCC CTG ACA AGC CTC ATA GCG AAG ATC CTT GAG Leu Ile Val Asn Ile Ser Leu Thr Ser Leu Ile Ala Lys Ile Leu Glu 1230 1235 1240	3926
40 TAT TCC GAC GTG GCG TCC ATC AAA GCC CTT CGG ACT CTC CGT GCC CTC Tyr Ser Asp Val Ala Ser Ile Lys Ala Leu Arg Thr Leu Arg Ala Leu 1245 1250 1255	3974
45 CGA CCG CTG CGG GCT CTG TCT CGA TTC GAA GGC ATG AGG GTA GTG GTG Arg Pro Leu Arg Ala Leu Ser Arg Phe Glu Gly Met Arg Val Val Val 1260 1265 1270	4022
50 TGC CTC ATC TTC TGG CTC ATC TTC AGC ATC ATG GGC GTG AAC CTC TTC Cys Leu Ile Phe Trp Leu Ile Phe Ser Ile Met Gly Val Asn Leu Phe 1290 1295 1300 1305	4118
55 GCC GGG AAA TTT TCG AAG TGC GTC GAC ACC AGA AAT AAC CCA TTT TCC Ala Gly Lys Phe Ser Lys Cys Val Asp Thr Arg Asn Asn Pro Phe Ser 1310 1315 1320	4166
60 AAC GTG AAT TCG ACG ATG GTG AAT AAC AAG TCC GAG TGT CAC AAT CAA Asn Val Asn Ser Thr Met Val Asn Asn Lys Ser Glu Cys His Asn Gln 1325 1330 1335	4214
AAC AGC ACC GGC CAC TTC TTC TGG GTC AAC GTC AAA GTC AAC TTC GAC Asn Ser Thr Gly His Phe Phe Trp Val Asn Val Lys Val Asn Phe Asp 1340 1345 1350	4262

AAC	GTC	GCT	ATG	GGC	TAC	CTC	GCA	CTT	CTT	CAG	GTG	GCA	ACC	TTC	AAA	4310	
Asn	Val	Ala	Met	Gly	Tyr	Leu	Ala	Leu	Leu	Gln	Val	Ala	Thr	Phe	Lys		
1355						1360					1365						
5	GGC	TGG	ATG	GAC	ATA	ATG	TAT	GCA	GCT	GTT	GAT	TCC	GGA	GAG	ATC	AAC	4358
	Gly	Trp	Met	Asp	Ile	Met	Tyr	Ala	Ala	Val	Asp	Ser	Gly	Glu	Ile	Asn	
	1370				1375					1380					1385		
10	AGT	CAG	CCT	AAC	TGG	GAG	AAC	AAC	TTG	TAC	ATG	TAC	CTG	TAC	TTC	GTC	4406
	Ser	Gln	Pro	Asn	Trp	Glu	Asn	Asn	Leu	Tyr	Met	Tyr	Leu	Tyr	Phe	Val	
					1390				1395					1400			
15	GTT	TTC	ATC	ATT	TTC	GGT	GGC	TTC	TTC	ACG	CTG	AAT	CTC	TTT	GTT	GGG	4454
	Val	Phe	Ile	Ile	Phe	Gly	Gly	Phe	Phe	Thr	Leu	Asn	Leu	Phe	Val	Gly	
					1405				1410					1415			
20	GTC	ATA	ATC	GAC	AAC	TTC	AAC	CAA	CAG	AAA	AAA	AAG	CTA	GGA	GGC	CAG	4502
	Val	Ile	Ile	Asp	Asn	Phe	Asn	Gln	Gln	Lys	Lys	Lys	Leu	Gly	Gly	Gln	
					1420			1425				1430					
25	GAC	ATC	TTC	ATG	ACA	GAA	GAG	CAG	AAG	AAG	TAC	TAC	AAT	GCC	ATG	AAG	4550
	Asp	Ile	Phe	Met	Thr	Glu	Glu	Gln	Lys	Lys	Tyr	Tyr	Asn	Ala	Met	Lys	
					1435			1440				1445					
30	AAG	CTG	GGC	TCC	AAG	AAA	CCC	CAG	AAG	CCC	ATC	CCA	CGG	CCC	CTG	AAT	4598
	Lys	Leu	Gly	Ser	Lys	Lys	Pro	Gln	Lys	Pro	Ile	Pro	Arg	Pro	Leu	Asn	
					1450			1455			1460				1465		
35	AAG	TAC	CAA	GGC	TTC	GTG	TTT	GAC	ATC	GTG	ACC	AGG	CAA	GCC	TTT	GAC	4646
	Lys	Tyr	Gln	Gly	Phe	Val	Phe	Asp	Ile	Val	Thr	Arg	Gln	Ala	Phe	Asp	
					1470			1475			1480						
40	ATC	ATC	ATC	ATG	GTT	CTC	ATC	TGC	CTC	AAC	ATG	ATC	ACC	ATG	ATG	GTG	4694
	Ile	Ile	Ile	Met	Val	Ile	Cys	Leu	Asn	Met	Ile	Thr	Met	Met	Val		
					1485			1490			1495						
45	GAG	ACC	GAC	GAG	CAG	GGC	GAG	AAG	ACG	AAG	GTT	CTG	GGC	AGA	ATC	4742	
	Glu	Thr	Asp	Glu	Gln	Gly	Glu	Glu	Lys	Thr	Lys	Val	Leu	Gly	Arg	Ile	
					1500			1505			1510						
50	AAC	CAG	TTC	TTT	GTG	GCC	GTC	TTC	ACG	GGC	GAG	TGT	GTG	ATG	AAG	ATG	4790
	Asn	Gln	Phe	Phe	Val	Ala	Val	Phe	Thr	Gly	Glu	Cys	Val	Met	Lys	Met	
					1515			1520			1525						
55	TTC	GCC	CTG	CGA	CAG	TAC	TAC	TTC	ACC	AAC	GGC	TGG	AAC	GTG	TTC	GAC	4838
	Phe	Ala	Leu	Arg	Gln	Tyr	Tyr	Phe	Thr	Asn	Gly	Trp	Asn	Val	Phe	Asp	
					1530			1535			1540				1545		
60	TTC	ATA	GTG	GTG	ATC	CTG	TCC	ATT	GGG	AGT	CTG	CTG	TTT	TCT	GCA	ATC	4886
	Phe	Ile	Val	Val	Ile	Leu	Ser	Ile	Gly	Ser	Leu	Leu	Phe	Ser	Ala	Ile	
					1550			1555			1560						
65	CTT	AAG	TCA	CTG	GAA	AAC	TAC	TTC	TCC	CCG	ACG	CTC	TTC	CGG	GTC	ATC	4934
	Leu	Lys	Ser	Leu	Glu	Asn	Tyr	Phe	Ser	Pro	Thr	Leu	Phe	Arg	Val	Ile	
					1565			1570			1575						
70	CGT	CTG	GCC	AGG	ATC	GGC	CGC	ATC	CTC	AGG	CTG	ATC	CGA	GCA	GCC	AAG	4982
	Arg	Leu	Ala	Arg	Ile	Gly	Arg	Ile	Leu	Arg	Leu	Ile	Arg	Ala	Ala	Lys	
					1580			1585			1590						
75	GGG	ATT	CGC	ACG	CTG	CTC	TTC	GCC	CTC	ATG	ATG	TCC	CTG	CCC	GCC	CTC	5030
	Gly	Ile	Arg	Thr	Leu	Leu	Phe	Ala	Leu	Met	Met	Ser	Leu	Pro	Ala	Leu	
					1595			1600			1605						

70086

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	TTC AAC ATC GGC CTC CTC TTC CTC GTC ATG TTC ATC TAC TCC ATC Phe Asn Ile Gly Leu Leu Phe Leu Val Met Phe Ile Tyr Ser Ile 1610 1615 1620 1625	5078
5	TTC GGC ATG GCC AGC TTC GCT AAC GTC GTG GAC GAG GCC GGC ATC GAC Phe Gly Met Ala Ser Phe Ala Asn Val Val Asp Glu Ala Gly Ile Asp 1630 1635 1640	5126
10	GAC ATG TTC AAC TTC AAG ACC TTT GGC AAC AGC ATG CTG TGC CTG TTC Asp Met Phe Asn Phe Lys Thr Phe Gly Asn Ser Met Leu Cys Leu Phe 1645 1650 1655	5174
15	CAG ATC ACC ACC TCG GCC GGC TGG GAC GGC CTC CTC AGC CCC ATC CTC Gln Ile Thr Thr Ser Ala Gly Trp Asp Gly Leu Leu Ser Pro Ile Leu 1660 1665 1670	5222
20	AAC ACG GGG CCT CCC TAC TGC GAC CCC AAC CTG CCC AAC AGC AAC GGC Asn Thr Gly Pro Pro Tyr Cys Asp Pro Asn Leu Pro Asn Ser Asn Gly 1675 1680 1685	5270
25	TCC CGG GGG AAC TGC GGG AGC CCG GCG GTG GGC ATC ATC TTC ACC Ser Arg Gly Asn Cys Gly Ser Pro Ala Val Gly Ile Ile Phe Phe Thr 1690 1695 1700 1705	5318
30	ACC TAC ATC ATC ATC TCC TTC CTC ATC GTG GTC AAC ATG TAC ATC GCA Thr Tyr Ile Ile Ser Phe Leu Ile Val Val Asn Met Tyr Ile Ala 1710 1715 1720	5366
35	GTG ATT CTG GAG AAC TTC AAC GTA GCC ACC GAG GAG AGC ACG GAG CCC Val Ile Leu Glu Asn Phe Asn Val Ala Thr Glu Glu Ser Thr Glu Pro 1725 1730 1735	5414
40	CTG AGC GAG GAC GAC TTC GAC ATG TTC TAT GAG ACC TGG GAG AAG TTC Leu Ser Glu Asp Asp Phe Asp Met Phe Tyr Glu Thr Trp Glu Lys Phe 1740 1745 1750	5462
45	GAC CCG GAG GCC ACC CAG TTC ATT GCC TTT TCT GCC CTC TCA GAC TTC Asp Pro Glu Ala Thr Gln Phe Ile Ala Phe Ser Ala Leu Ser Asp Phe 1755 1760 1765	5510
50	GCG GAC ACG CTC TCC GGC CCT CTT AGA ATC CCC AAA CCC AAC CAG AAT Ala Asp Thr Leu Ser Gly Pro Leu Arg Ile Pro Lys Pro Asn Gln Asn 1770 1775 1780 1785	5558
55	ATA TTA ATC CAG ATG GAC CTG CCG TTG GTC CCC GGG GAT AAG ATC CAC Ile Leu Ile Gln Met Asp Leu Pro Leu Val Pro Gly Asp Lys Ile His 1790 1795 1800	5606
60	TGT CTG GAC ATC CTT TTT GCC TTC ACA AAG AAC GTC TTG GGA GAA TCC Cys Leu Asp Ile Leu Phe Ala Phe Thr Lys Asn Val Leu Gly Glu Ser 1805 1810 1815	5654
	GGG GAG TTG GAC TCC CTG AAG ACC AAT ATG GAA GAG AAG TTT ATG GCG Gly Glu Leu Asp Ser Leu Lys Thr Asn Met Glu Glu Lys Phe Met Ala 1820 1825 1830	5702
	ACC AAT CTC TCC AAA GCA TCC TAT GAA CCA ATA GCC ACC ACC CTC CGG Thr Asn Leu Ser Lys Ala Ser Tyr Glu Pro Ile Ala Thr Thr Leu Arg 1835 1840 1845	5750
	TGG AAG CAG GAA GAC CTC TCA GCC ACA GTC ATT CAA AAG GCC TAC CGG Trp Lys Gln Glu Asp Leu Ser Ala Thr Val Ile Gln Lys Ala Tyr Arg 1850 1855 1860	5798

AGC TAC ATG CTG CAC CGC TCC TTG ACA CTC TCC AAC ACC CTG CAT GTG Ser Tyr Met Leu His Arg Ser Leu Thr Leu Ser Asn Thr Leu His Val 1870 1875 1880	5846
5 CCC AGG GCT GAG GAG GAT GGC GTG TCA CTT CCC GGG GAA GGC TAC AGT Pro Arg Ala Glu Glu Asp Gly Val Ser Leu Pro Gly Glu Gly Tyr Ser 1885 1890 1895	5894
10 ACA TTC ATG GCA AAC ACT GGA CTC CCG GAC AAA TCA GAA ACT GCC TCT Thr Phe Met Ala Asn Ser Gly Leu Pro Asp Lys Ser Glu Thr Ala Ser 1900 1905 1910	5942
15 GCT ACG TCT TTC CCG CCA TCC TAT GAC AGT GTC ACC AGG GGC CTG AGT Ala Thr Ser Phe Pro Pro Ser Tyr Asp Ser Val Thr Arg Gly Leu Ser 1915 1920 1925	5990
20 GAC CGG GCC AAC ATT AAC CCA TCT AGC TCA ATG CAA AAT GAA GAT GAG Asp Arg Ala Asn Ile Asn Pro Ser Ser Met Gln Asn Glu Asp Glu 1930 1935 1940 1945	6038
25 GTC GCT AAG GAA GGA AAC AGC CCT GGA CCT CAG TGAAAGGCAGT Val Ala Ala Lys Glu Gly Asn Ser Pro Gly Pro Gln 1950 1955	6084
30 CAGGCATGCA CAGGGCAGGT TCCAATGTCT TTCTCTGCTG TACTAACTCC TTCCCTCTGG AGGTGGCACCC AACCTCCAGC CTCCACCAAT GCATGTCACT GGTCATGGTG TCAGAACTGA	6144
35 ATGGGGACAT CCTTGAGAAA GCCCCCACCC CAATAGGAAT CAAAAGCCAA GGATACTCCT CCATTCTGAC GTCCCTTCCG AGTTCCCAGA AGATGTGATT GCTCCCTTCT GTTTGTGACC	6204
40 AGAGACGTGA TTCACCAACT TCTCGGAGCC AGAGACACAT AGCAAAGACT TTTCTGCTGG TGTCGGGCAG TCTTAGAGAA GTCACGTAGG GGTTGGTACT GAGAATTAGG GTTTGCATGA CTGCATGCTC ACAGCTGCCG GACAATACCT GTGAGTCGGC CATTAAAATT AATATTTTA AAGTTAAAAA AAAAAAAA AAA	6264
	6324
	6384
	6444
	6504
	6527

(2) INFORMATION FOR SEQ ID NO:8:

- 45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1957 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
- 50 (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Glu Leu Pro Phe Ala Ser Val Gly Thr Thr Asn Phe Arg Arg Phe 1 5 10 15	
55 Thr Pro Glu Ser Leu Ala Glu Ile Glu Lys Gln Ile Ala Ala His Arg 20 25 30	
60 Ala Ala Lys Lys Ala Arg Thr Lys His Arg Gly Gln Glu Asp Lys Gly 35 40 45	
Glu Lys Pro Arg Pro Gln Leu Asp Leu Lys Asp Cys Asn Gln Leu Pro 50 55 60	

Lys Phe Tyr Gly Glu Leu Pro Ala Glu Leu Val Gly Glu Pro Leu Glu
 65 70 75 80

Asp Leu Asp Pro Phe Tyr Ser Thr His Arg Thr Phe Met Val Leu Asn
 5 85 90 95

Lys Ser Arg Thr Ile Ser Arg Phe Ser Ala Thr Trp Ala Leu Trp Leu
 100 105 110

Phe Ser Pro Phe Asn Leu Ile Arg Arg Thr Ala Ile Lys Val Ser Val
 115 120 125

His Ser Trp Phe Ser Ile Phe Ile Thr Ile Thr Ile Leu Val Asn Cys
 130 135 140

Val Cys Met Thr Arg Thr Asp Leu Pro Glu Lys Val Glu Tyr Val Phe
 145 150 155 160

Thr Val Ile Tyr Thr Phe Glu Ala Leu Ile Lys Ile Leu Ala Arg Gly
 20 165 170 175

Phe Cys Leu Asn Glu Phe Thr Tyr Leu Arg Asp Pro Trp Asn Trp Leu
 180 185 190

Asp Phe Ser Val Ile Thr Leu Ala Tyr Val Gly Ala Ala Ile Asp Leu
 25 195 200 205

Arg Gly Ile Ser Gly Leu Arg Thr Phe Arg Val Leu Arg Ala Leu Lys
 210 215 220

Thr Val Ser Val Ile Pro Gly Leu Lys Val Ile Val Gly Ala Leu Ile
 30 225 230 235 240

His Ser Val Arg Lys Leu Ala Asp Val Thr Ile Leu Thr Val Phe Cys
 35 245 250 255

Leu Ser Val Phe Ala Leu Val Gly Leu Gln Leu Phe Lys Gly Asn Leu
 260 265 270

Lys Asn Lys Cys Ile Arg Asn Gly Thr Asp Pro His Lys Ala Asp Asn
 40 275 280 285

Leu Ser Ser Glu Met Ala Glu Tyr Ile Phe Ile Lys Pro Gly Thr Thr
 45 290 295 300

Asp Pro Leu Leu Cys Gly Asn Gly Ser Asp Ala Gly His Cys Pro Gly
 305 310 315 320

Gly Tyr Val Cys Leu Lys Thr Pro Asp Asn Pro Asp Phe Asn Tyr Thr
 50 325 330 335

Ser Phe Asp Ser Phe Ala Trp Ala Phe Leu Ser Leu Phe Arg Leu Met
 340 345 350

Thr Gln Asp Ser Trp Glu Arg Leu Tyr Gln Gln Thr Leu Arg Ala Ser
 55 355 360 365

Gly Lys Met Tyr Met Val Phe Phe Val Leu Val Ile Phe Leu Gly Ser
 60 370 375 380

Phe Tyr Leu Val Asn Leu Ile Leu Ala Val Val Thr Met Ala Tyr Glu
 385 390 395 400

Glu Gln Ser Gln Ala Thr Ile Ala Glu Ile Glu Ala Lys Glu Lys Lys
405 410 415

5 Phe Gln Glu Ala Leu Glu Val Leu Gln Lys Glu Gln Glu Val Leu Ala
420 425 430

Ala Leu Gly Ile Asp Thr Thr Ser Leu Gln Ser His Ser Gly Ser Pro
435 440 445

10 Leu Ala Ser Lys Asn Ala Asn Glu Arg Arg Pro Arg Val Lys Ser Arg
450 455 460

Val Ser Glu Gly Ser Thr Asp Asp Asn Arg Ser Pro Gln Ser Asp Pro
465 470 475 480

15 Tyr Asn Gln Arg Arg Met Ser Phe Leu Gly Leu Ser Ser Gly Arg Arg
485 490 495

Arg Ala Ser His Gly Ser Val Phe His Phe Arg Ala Pro Ser Gln Asp
20 500 505 510

Ile Ser Phe Pro Asp Gly Ile Thr Pro Asp Asp Gly Val Phe His Gly
515 520 525

25 Asp Gln Glu Ser Arg Arg Gly Ser Ile Leu Leu Gly Arg Gly Ala Gly
530 535 540

Gln Thr Gly Pro Leu Pro Arg Ser Pro Leu Pro Gln Ser Pro Asn Pro
545 550 555 560

30 Gly Arg Arg His Gly Glu Gly Gln Leu Gly Val Pro Thr Gly Glu
565 570 575

Leu Thr Ala Gly Ala Pro Glu Gly Pro Ala Leu Asp Thr Thr Gly Gln
35 580 585 590

Lys Ser Phe Leu Ser Ala Gly Tyr Ile Asn Glu Pro Phe Arg Ala Gln
595 600 605

40 Arg Ala Met Ser Val Val Ser Ile Met Thr Ser Val Ile Glu Glu Leu
610 615 620

Glu Glu Ser Lys Leu Lys Cys Pro Pro Cys Leu Ile Ser Phe Ala Gln
625 630 635 640

45 Lys Tyr Leu Ile Trp Glu Cys Cys Pro Lys Trp Arg Lys Phe Lys Met
645 650 655

50 Ala Leu Phe Glu Leu Val Thr Asp Pro Phe Ala Glu Leu Thr Ile Thr
660 665 670

Leu Cys Ile Val Val Asn Thr Val Phe Met Ala Met Glu His Tyr Pro
675 680 685

55 Met Thr Asp Ala Phe Asp Ala Met Leu Gln Ala Gly Asn Ile Val Phe
690 695 700

Thr Val Phe Phe Thr Met Glu Met Ala Phe Lys Ile Ile Ala Phe Asp
705 710 715 720

60 Pro Tyr Tyr Tyr Phe Gln Lys Lys Trp Asn Ile Phe Asp Cys Val Ile
725 730 735

Val Thr Val Ser Leu Leu Glu Leu Ser Ala Ser Lys Lys Gly Ser Leu
 740 745 750
 Ser Val Leu Arg Ser Leu Arg Leu Leu Arg Val Phe Lys Leu Ala Lys
 5 755 760 765
 Ser Trp Pro Thr Deu Asn Thr Leu Ile Lys Ile Ile Gly Asn Ser Val
 770 775 780
 Gly Ala Leu Gly Asn Leu Thr Phe Ile Leu Ala Ile Ile Val Phe Ile
 10 785 790 795 800
 Phe Ala Leu Val Gly Lys Gln Leu Leu Ser Glu Asp Tyr Gly Cys Arg
 805 810 815
 15 Lys Asp Gly Val Ser Val Trp Asn Gly Glu Lys Leu Arg Trp His Met
 820 825 830
 Cys Asp Phe Phe His Ser Phe Leu Val Val Phe Arg Ile Leu Cys Gly
 20 835 840 845
 Glu Trp Ile Glu Asn Met Trp Val Cys Met Glu Val Ser Gln Lys Ser
 850 855 860
 Ile Cys Leu Ile Leu Phe Leu Thr Val Met Val Leu Gly Asn Leu Val
 25 865 870 875 880
 Val Leu Asn Leu Phe Ile Ala Leu Leu Leu Asn Ser Phe Ser Ala Asp
 30 885 890 895
 Asn Leu Thr Ala Pro Glu Asp Asp Gly Glu Val Asn Asn Leu Gln Leu
 900 905 910
 Ala Leu Ala Arg Ile Gln Val Leu Gly His Arg Ala Ser Arg Ala Ile
 35 915 920 925
 Ala Ser Tyr Ile Ser Ser His Cys Arg Phe Arg Trp Pro Lys Val Glu
 930 935 940
 Thr Gln Leu Gly Met Lys Pro Pro Leu Thr Ser Ser Glu Ala Lys Asn
 40 945 950 955 960
 His Ile Ala Thr Asp Ala Val Ser Ala Ala Val Gly Asn Leu Thr Lys
 45 965 970 975
 Pro Ala Leu Ser Ser Pro Lys Glu Asn His Gly Asp Phe Ile Thr Asp
 980 985 990
 Pro Asn Val Trp Val Ser Val Pro Ile Ala Glu Gly Glu Ser Asp Leu
 50 995 1000 1005
 Asp Glu Leu Glu Glu Asp Met Glu Gln Ala Ser Gln Ser Ser Trp Gln
 1010 1015 1020
 Glu Glu Asp Pro Lys Gly Gln Gln Glu Gln Leu Pro Gln Val Gln Lys
 55 1025 1030 1035 1040
 Cys Glu Asn His Gln Ala Ala Arg Ser Pro Ala Ser Met Met Ser Ser
 1045 1050 1055
 60 Glu Asp Leu Ala Pro Tyr Leu Gly Glu Ser Trp Lys Arg Lys Asp Ser
 1060 1065 1070

Pro Gln Val Pro Ala Glu Gly Val Asp Asp Thr Ser Ser Ser Glu Gly
1075 1080 1085

Ser Thr Val Asp Cys Pro Asp Pro Glu Glu Ile Leu Arg Lys Ile Pro
5 1090 1095 1100

Glu Leu Ala Asp Asp Leu Asp Glu Pro Asp Asp Cys Phe Thr Glu Gly
1105 1110 1115 1120

Cys Thr Arg Arg Cys Pro Cys Cys Asn Val Asn Thr Ser Lys Ser Pro
10 1125 1130 1135

Trp Ala Thr Gly Trp Gln Val Arg Lys Thr Cys Tyr Arg Ile Val Glu
1140 1145 1150

His Ser Trp Phe Glu Ser Phe Ile Ile Phe Met Ile Leu Leu Ser Ser
15 1155 1160 1165

Gly Ala Leu Ala Phe Glu Asp Asn Tyr Leu Glu Glu Lys Pro Arg Val
20 1170 1175 1180

Lys Ser Val Leu Glu Tyr Thr Asp Arg Val Phe Thr Phe Ile Phe Val
1185 1190 1195 1200

Phe Glu Met Leu Leu Lys Trp Val Ala Tyr Gly Phe Lys Lys Tyr Phe
25 1205 1210 1215

Thr Asn Ala Trp Cys Trp Leu Asp Phe Leu Ile Val Asn Ile Ser Leu
1220 1225 1230

Thr Ser Leu Ile Ala Lys Ile Leu Glu Tyr Ser Asp Val Ala Ser Ile
30 1235 1240 1245

Lys Ala Leu Arg Thr Leu Arg Ala Leu Arg Pro Leu Arg Ala Leu Ser
35 1250 1255 1260

Arg Phe Glu Gly Met Arg Val Val Val Asp Ala Leu Val Gly Ala Ile
1265 1270 1275 1280

Pro Ser Ile Met Asn Val Leu Leu Val Cys Leu Ile Phe Trp Leu Ile
40 1285 1290 1295

Phe Ser Ile Met Gly Val Asn Leu Phe Ala Gly Lys Phe Ser Lys Cys
45 1300 1305 1310

Val Asp Thr Arg Asn Asn Pro Phe Ser Asn Val Asn Ser Thr Met Val
1315 1320 1325

Asn Asn Lys Ser Glu Cys His Asn Gln Asn Ser Thr Gly His Phe Phe
50 1330 1335 1340 1345

Trp Val Asn Val Lys Val Asn Phe Asp Asn Val Ala Met Gly Tyr Leu
1350 1355 1360

Ala Leu Leu Gln Val Ala Thr Phe Lys Gly Trp Met Asp Ile Met Tyr
55 1365 1370 1375

Ala Ala Val Asp Ser Gly Glu Ile Asn Ser Gln Pro Asn Trp Glu Asn
60 1380 1385 1390

Asn Leu Tyr Met Tyr Leu Tyr Phe Val Val Phe Ile Ile Phe Gly Gly
1395 1400 1405

Phe Phe Thr Leu Asn Leu Phe Val Gly Val Ile Ile Asp Asn Phe Asn
 1410 1415 1420
 Gln Gln Lys Lys Lys Leu Gly Gly Gln Asp Ile Phe Met Thr Glu Glu
 5 1425 1430 1435 1440
 Gln Lys Lys Tyr Tyr Asn Ala Met Lys Lys Leu Gly Ser Lys Lys Pro
 1445 1450 1455
 10 Gln Lys Pro Ile Pro Arg Pro Leu Asn Lys Tyr Gln Gly Phe Val Phe
 1460 1465 1470
 Asp Ile Val Thr Arg Gln Ala Phe Asp Ile Ile Ile Met Val Leu Ile
 1475 1480 1485
 15 Cys Leu Asn Met Ile Thr Met Met Val Glu Thr Asp Glu Gln Gly Glu
 1490 1495 1500
 Glu Lys Thr Lys Val Leu Gly Arg Ile Asn Gln Phe Phe Val Ala Val
 20 1505 1510 1515 1520
 Phe Thr Gly Glu Cys Val Met Lys Met Phe Ala Leu Arg Gln Tyr Tyr
 1525 1530 1535
 25 Phe Thr Asn Gly Trp Asn Val Phe Asp Phe Ile Val Val Ile Leu Ser
 1540 1545 1550
 Ile Gly Ser Leu Leu Phe Ser Ala Ile Leu Lys Ser Leu Glu Asn Tyr
 30 1555 1560 1565
 Phe Ser Pro Thr Leu Phe Arg Val Ile Arg Leu Ala Arg Ile Gly Arg
 1570 1575 1580
 Ile Leu Arg Leu Ile Arg Ala Ala Lys Gly Ile Arg Thr Leu Leu Phe
 35 1585 1590 1595 1600
 Ala Leu Met Met Ser Leu Pro Ala Leu Phe Asn Ile Gly Leu Leu Leu
 1605 1610 1615
 40 Phe Leu Val Met Phe Ile Tyr Ser Ile Phe Gly Met Ala Ser Phe Ala
 1620 1625 1630
 Asn Val Val Asp Glu Ala Gly Ile Asp Asp Met Phe Asn Phe Lys Thr
 45 1635 1640 1645
 Phe Gly Asn Ser Met Leu Cys Leu Phe Gln Ile Thr Thr Ser Ala Gly
 1650 1655 1660
 Trp Asp Gly Leu Leu Ser Pro Ile Leu Asn Thr Gly Pro Pro Tyr Cys
 50 1665 1670 1675 1680
 Asp Pro Asn Leu Pro Asn Ser Asn Gly Ser Arg Gly Asn Cys Gly Ser
 1685 1690 1695
 55 Pro Ala Val Gly Ile Ile Phe Phe Thr Thr Tyr Ile Ile Ile Ser Phe
 1700 1705 1710
 Leu Ile Val Val Asn Met Tyr Ile Ala Val Ile Leu Glu Asn Phe Asn
 60 1715 1720 1725
 Val Ala Thr Glu Glu Ser Thr Glu Pro Leu Ser Glu Asp Asp Phe Asp
 1730 1735 1740

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Met Phe Tyr Glu Thr Trp Glu Lys Phe Asp Pro Glu Ala Thr Gln Phe
1745 1750 1755 1760

Ile Ala Phe Ser Ala Leu Ser Asp Phe Ala Asp Thr Leu Ser Gly Pro
5 1765 1770 1775

Leu Arg Ile Pro Lys Pro Asn Gln Asn Ile Leu Ile Gln Met Asp Leu
1780 1785 1790

Pro Leu Val Pro Gly Asp Lys Ile His Cys Leu Asp Ile Leu Phe Ala
10 1795 1800 1805

Phe Thr Lys Asn Val Leu Gly Glu Ser Gly Glu Leu Asp Ser Leu Lys
1810 1815 1820

15 Thr Asn Met Glu Glu Lys Phe Met Ala Thr Asn Leu Ser Lys Ala Ser
1825 1830 1835 1840

Tyr Glu Pro Ile Ala Thr Thr Leu Arg Trp Lys Gln Glu Asp Leu Ser
20 1845 1850 1855

Ala Thr Val Ile Gln Lys Ala Tyr Arg Ser Tyr Met Leu His Arg Ser
1860 1865 1870

Leu Thr Leu Ser Asn Thr Leu His Val Pro Arg Ala Glu Glu Asp Gly
25 1875 1880 1885

Val Ser Leu Pro Gly Glu Gly Tyr Ser Thr Phe Met Ala Asn Ser Gly
30 1890 1895 1900

Leu Pro Asp Lys Ser Glu Thr Ala Ser Ala Thr Ser Phe Pro Pro Ser
1905 1910 1915 1920

Tyr Asp Ser Val Thr Arg Gly Leu Ser Asp Arg Ala Asn Ile Asn Pro
35 1925 1930 1935

Ser Ser Ser Met Gln Asn Glu Asp Glu Val Ala Ala Lys Glu Gly Asn
40 1940 1945 1950

(2) INFORMATION FOR SEQ ID NO:9:

45 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
50 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CAGCTTCGCT CAGAAAGTATC T

21

60 (2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: cDNA

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

10 TTCTCGCCGT TCCACACGGGA GA

22

(2) INFORMATION FOR SEQ ID NO:11:

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: peptide

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

25 Phe Arg Leu Met
1

(2) INFORMATION FOR SEQ ID NO:12:

30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

35 (ii) MOLECULE TYPE: peptide

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

40 Thr Gln Asp Phe Trp Glu Asn Leu Tyr
1 5

45 (2) INFORMATION FOR SEQ ID NO:13:

45 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

50 (ii) MOLECULE TYPE: peptide

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

55 Thr Gln Asp Tyr Trp Glu Asn Leu Tyr
1 5

60 (2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9 amino acids

(B) TYPE: amino acid
(D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

10 Thr Gln Asp Cys Trp Glu Arg Leu Tyr
1 5

(2) INFORMATION FOR SEQ ID NO:15:

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

25 Thr Gln Asp Ser Trp Glu Arg Leu Tyr
1 5

(2) INFORMATION FOR SEQ ID NO:16:

30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

35 (ii) MOLECULE TYPE: peptide

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Thr Gln Asp Phe Trp Glu Arg Leu Tyr
1 5

45 (2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
50 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Thr Gln Asp Ser Trp Glu Arg
1 5

60 (2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids

(B) TYPE: amino acid
(D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: peptide

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Gly Ser Thr Asp Asp Asn Arg Ser Pro Gln Ser Asp Pro Tyr Asn
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:19:

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: peptide

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Ser Pro Lys Glu Asn His Gly Asp Phe Ile
1 5 10

30 (2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

35 (ii) MOLECULE TYPE: peptide

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Pro Asn His Asn Gly Ser Arg Gly Asn
1 5

45 (2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

50 (ii) MOLECULE TYPE: peptide

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Arg Leu Leu Arg Val Phe Lys Leu Ala Lys Ser Trp Pro Thr Leu
1 5 10 15

60 (2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs

- (B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: cDNA

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GCTTGCTGCG GGTCTTCAAG C

21

(2) INFORMATION FOR SEQ ID NO:23:

- 15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

25 Leu Arg Ala Leu Pro Leu Arg Ala Leu Ser Arg Phe Glu Gly
1 5 10

(2) INFORMATION FOR SEQ ID NO:24:

- 30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

35 (ii) MOLECULE TYPE: cDNA

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

ATCGAGACAG AGCCCGCAGC G

21

(2) INFORMATION FOR SEQ ID NO:25:

- 45 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 44 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

50 (ii) MOLECULE TYPE: cDNA

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

ACGGGTGCCG CAAGGACGGC GTCTCCGTGT GGAACGGCGA GAAG

44

60 (2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

10 GGCTATCCTT CCTCTTCCAG CTCTCACCCA GGTATGGAGC CAGGT

45

(2) INFORMATION FOR SEQ ID NO:27:

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: cDNA

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

25 TCCCCGTACGC TGCAGCTCTT T

21

(2) INFORMATION FOR SEQ ID NO:28:

30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

35 (ii) MOLECULE TYPE: cDNA

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

40 CCCGGGGAAG GCTAC

15

(2) INFORMATION FOR SEQ ID NO:29:

45 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

50 (ii) MOLECULE TYPE: cDNA

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

55 GTCGACACCA GAAAT

15

60 (2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: cDNA

10 10 GGATCCTCTA GAGTCGACCT GCAGAAGGAA

30

(2) INFORMATION FOR SEQ ID NO:31:

- 15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: cDNA

25 25 TGACGCCAGGA CTCCTGGGAG CGCC

24



CERTIFICATE OF MAILING (37 CFR 1.8 (a))

I hereby certify that the attached papers or fee is being deposited with the United States Postal Service on the date shown below with sufficient postage as first class mail in an envelope addressed to the: Assistant Commissioner For Patents, Washington, D.C. 20231.

January 21, 1997
(Date)

LIZA D. HOHENSCHUTZ
(Printed Name)

Liza D. Hohenschutz
(Signature)

ZENECA Inc.
Docket No. 70086

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Application of: WOOD ET AL.

Serial Number: 08/669,656

Group Art Unit:

Filed: JUNE 24, 1996

Examiner:

For: ION CHANNEL

Assistant Commissioner for Patents
Washington, D.C. 20231

Sir:

COVER LETTER

Transmitted herewith are the following:

- Response to Office Action.
- Petition for extension of time (37 CFR 1.136).
- Information Disclosure Statement.
- Information Disclosure Citation by Applicant (Form PTO-1449)
- Appeal Brief (in triplicate).
- Issue Fee (Forms PTOL -85B and -85C).
- 2 References

The items checked below are appropriate:

1. It is believed that no fee is due as a result of this transmittal.

2. (X) The Commissioner is hereby authorized to charge any additional fees which may be required or to credit any overpayment to Deposit Account No. 26-0166. This sheet is enclosed in duplicate.

Respectfully submitted,

ZENECA Inc.

Dated: January 21, 1997

ZENECA Inc.
Docket No. 70086
y:\ldh\70086\0117cov.doc

By: Liza D. Hohenschutz
Liza D. Hohenschutz
Attorney for Applicants
Reg. No. 33,712
Telephone: 302/886-7466



Application No.: 08669,652

NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING
NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

- 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to these regulations, published at 1114 OG 29, May 15, 1990 and at 55 FR 18230, May 1, 1990.
- 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).
- 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).
- 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked-up 'Raw Sequence Listing.'
- 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).
- 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).
- 7. Other: _____

Applicant Must Provide:

- An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".
- An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.
- A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216

For CRF Submission Help, call (703) 308-4212

For PatentIn software help, call (703) 308-6856

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